



SEQUENCE LISTING

<110> Parales, R.
Gibson, D.
Resnick, S.
Lee, K.

<120> Novel naphthalene dioxygenase and methods for their use

<130> 875.006US2

<140> US 09/843,250

<141> 2001-04-26

<150> PCT/US99/25079

<151> 1999-10-26

<150> US 60/105,575

<151> 1998-10-26

<160> 65

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 2265

<212> DNA

<213> Artificial Sequence

<220>

<223> A sequence encoding an NDO mutant.

<400> 1

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cgctttactc gctttatcac caacgtccag gccgcaatgg acgtaaatga caaagagcta		1980
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<210> 2

<211> 449

<212> PRT

<213> Artificial Sequence

<220>

<223> A polypeptide encoded by SEQ ID NO:1

<400> 2

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20	25	30	
Thr Ile Phe Ala Arg Asn Trp Leu Phe Leu Thr His Asp Ser Leu Ile			
35	40	45	
Pro Ala Pro Gly Asp Tyr Val Thr Ala Lys Met Gly Ile Asp Glu Val			
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Cys Arg His Arg Gly Lys Thr Leu Val Ser Val Glu Ala Gly Asn Ala			
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Glu Leu Gln Ser Val Pro Phe Glu Lys Asp Leu Tyr Gly Glu Ser Leu			
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Asn Lys Lys Cys Leu Gly Leu Lys Glu Val Ala Arg Val Glu Ser Phe			
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His Gly Phe Ile Tyr Gly Cys Phe Asp Gln Glu Ala Pro Pro Leu Met			
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Asp Tyr Leu Gly Asp Ala Ala Trp Tyr Leu Glu Pro Met Phe Lys His			
165	170	175	
Ser Gly Gly Leu Glu Leu Val Gly Pro Pro Gly Lys Val Val Ile Lys			
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Val Gly Trp Thr His Ala Ser Ser Leu Arg Ser Gly Glu Ser Ile Phe			
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Ser Met Leu Thr Cys Ser Gly Val Phe Lys Val Trp Asn Pro Ile Asp			
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Pro Glu Asp Leu Lys Arg Arg Leu Ala Asp Ser Val Gln Arg Thr Val			
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 Ala Ser Gln Asn Gly Lys Lys Tyr Gln Ser Arg Asp Ser Asp Leu Leu
 370 375 380
 Ser Asn Leu Gly Phe Gly Glu Asp Val Tyr Gly Asp Ala Val Tyr Pro
 385 390 395 400
 Gly Val Val Gly Lys Ser Ala Ile Gly Glu Thr Ser Tyr Arg Gly Phe
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 Tyr Arg Ala Tyr Gln Ala His Val Ser Ser Asn Trp Ala Glu Phe
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 Glu His Ala Ser Ser Thr Trp His Thr Glu Leu Thr Lys Thr Thr Asp
 435 440 445
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<210> 3
 <211> 9841
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> A modified DNA molecule encoding valine at the
 position corresponding to the F352 amino acid in
 NDO.

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<210> 4
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> A modified DNA molecule encoding valine at the position corresponding to the F352 amino acid in NDO.

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 <212> DNA
 <213> Artificial Sequence

<220>
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<221> misc_feature
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 <223> n = a or t or g or c

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<210> 7
 <211> 4355
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> A modified DNA molecule encoding valine at the position corresponding to the F352 amino acid in NDO.

<400> 7

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<210> 8
<211> 2176
<212> DNA
<213> Artificial Sequence
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<220>
<223> A modified DNA molecule encoding valine at the position corresponding to the F352 amino acid in NDO.

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<210> 9
<211> 14462
<212> DNA
<213> Artificial Sequence
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<220>
<223> A modified DNA molecule encoding valine at the

position corresponding to the F352 amino acid in
NDO.

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<223> A modified DNA molecule encoding valine at the position corresponding to the F352 amino acid in NDO.

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<211> 4912
<212> DNA

<213> Artificial Sequence

<220>

<223> A modified DNA molecule encoding valine at the position corresponding to the F352 amino acid in NDO.

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<210> 13

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<212> DNA

<213> Artificial Sequence

<220>

<223> A modified DNA molecule encoding valine at the position corresponding to the F352 amino acid in NDO.

<400> 13

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gogcaaaaca	ggaaaagct	gccaagaaaa	tcggcgatgt	ccggggcgccgg	atttaccgc	4740
gccaaagt	cgccacgg	ttcccgaaaca	actgcgtttt	gaccggcgcc	ggtgtcttca	4800
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aataccaatc	cagcaacagt	gatctgattt	ccgatttggg	tttcggcaag	gacgtctacg	5040

gcgacgaatg	ctatccggc	gtcgtagca	aatcgccatt	cagcgaaacc	aaccatcg	5100
gatttac	cg	gtcacatca	gcagctcaa	ttggccgag	ttcgaaaaca	5160
cctccc	aaa	ttggcacacc	gaactcacca	agacgactga	tcgctaattc	5220
catgatgatc	aatacc	cagg	aagacaagct	ggtctccg	cacgacgccc	5280
ccgttcttc	gtc	gggac	acagcgat	gcagcaagaa	gtcaccacac	5340
cgaagccgac	ctg	ctggaca	ttcaggc	caaagc	tttgaacact	5400
cgagatcaa	aa	tacca	actcg	cttccg	gacgatacc	5460
actgaatgat	gcgg	taata	actat	cagctgaa	ttcgagt	5520
acaccagatg	atc	cctc	aga	cgttca	cccgtt	5580
caccaatgtc	acgg	ccggca	aggaca	cgcc	atcgcttca	5640
cctcattctc	catc	gccc	gacgagg	ccaag	gtcttctat	5700
agacaaatgg	aa	acgc	aagg	tttca	gtcaacg	5760
cccgagcgc	ag	cccc	ccacaa	ac	ttgttgc	5820
tgccctggat	gcgg	gattt	ttaa	cagg	ggat	5880
acaccctgga	ttt	cagt	tgag	gtg	ctatt	5940
gtagaccg	ac	gggt	gtat	ccctt	ggcc	6000
ggcaatcg	tc	gagct	gtgt	tttcc	tggg	6060
ctggc	gacc	aggc	attca	tgt	gatccc	6120
gcaga	gtac	acgg	ctat	ggag	tgt	6180
gcctc	gg	tttgc	actg	actt	catgg	6240
gaaggc	ctgc	tttt	ccaa	ccat	atgccc	6300
cacc	ccgg	ctgg	cggc	tttgc	gctt	6360
gatg	agat	ccct	ggaa	tttgc	tttgc	6420
atgg	atgc	tttt	ctgg	tttgc	tttgc	6480
ccg	ttgt	ttgg	gtgg	tttgc	tttgc	6540
catgg	catag	atgc	atgtt	tttgc	tttgc	6600
ata	caaac	gttca	ggcaat	tttgc	tttgc	6660
gatc	cacc	aggc	actcg	tttgc	tttgc	6720
tct	geg	ctgc	aggact	tttgc	tttgc	6779

<210> 14
 <211> 449
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> A polypeptide encoded by SEQ ID NO:3.

<400> 14
 Met Asn Tyr Asn Asn Lys Ile Leu Val Ser Glu Ser Gly Leu Ser Gln
 1 5 10 15
 Lys His Leu Ile His Gly Asp Glu Glu Leu Phe Gln His Glu Leu Lys
 20 25 30
 Thr Ile Phe Ala Arg Asn Trp Leu Phe Leu Thr His Asp Ser Leu Ile
 35 40 45
 Pro Ala Pro Gly Asp Tyr Val Thr Ala Lys Met Gly Ile Asp Glu Val
 50 55 60
 Ile Val Ser Arg Gln Asn Asp Gly Ser Ile Arg Ala Phe Leu Asn Val
 65 70 75 80
 Cys Arg His Arg Gly Lys Thr Leu Val Ser Val Glu Ala Gly Asn Ala
 85 90 95
 Lys Gly Phe Val Cys Ser Tyr His Gly Trp Gly Phe Gly Ser Asn Gly
 100 105 110
 Glu Leu Gln Ser Val Pro Phe Glu Lys Asp Leu Tyr Gly Glu Ser Leu
 115 120 125
 Asn Lys Lys Cys Leu Gly Leu Lys Glu Val Ala Arg Val Glu Ser Phe
 130 135 140
 His Gly Phe Ile Tyr Gly Cys Phe Asp Gln Glu Ala Pro Pro Leu Met
 145 150 155 160

Asp Tyr Leu Gly Asp Ala Ala Trp Tyr Leu Glu Pro Met Phe Lys His
 165 170 175
 Ser Gly Gly Leu Glu Leu Val Gly Pro Pro Gly Lys Val Val Ile Lys
 180 185 190
 Ala Asn Trp Lys Ala Pro Ala Glu Asn Phe Val Gly Asp Ala Tyr His
 195 200 205
 Val Gly Trp Thr His Ala Ser Ser Leu Arg Ser Gly Glu Ser Ile Phe
 210 215 220
 Ser Ser Leu Ala Gly Asn Ala Ala Leu Pro Pro Glu Gly Ala Gly Leu
 225 230 235 240
 Gln Met Thr Ser Lys Tyr Gly Ser Gly Met Gly Val Leu Trp Asp Gly
 245 250 255
 Tyr Ser Gly Val His Ser Ala Asp Leu Val Pro Glu Leu Met Ala Phe
 260 265 270
 Gly Gly Ala Lys Gln Glu Arg Leu Asn Lys Glu Ile Gly Asp Val Arg
 275 280 285
 Ala Arg Ile Tyr Arg Ser His Leu Asn Cys Thr Val Phe Pro Asn Asn
 290 295 300
 Ser Met Leu Thr Cys Ser Gly Val Phe Lys Val Trp Asn Pro Ile Asp
 305 310 315 320
 Ala Asn Thr Thr Glu Val Trp Thr Tyr Ala Ile Val Glu Lys Asp Met
 325 330 335
 Pro Glu Asp Leu Lys Arg Arg Leu Ala Asp Ser Val Gln Arg Thr Val
 340 345 350
 Gly Pro Ala Gly Phe Trp Glu Ser Asp Asp Asn Asn Met Glu Thr
 355 360 365
 Ala Ser Gln Asn Gly Lys Tyr Gln Ser Arg Asp Ser Asp Leu Leu
 370 375 380
 Ser Asn Leu Gly Phe Gly Glu Asp Val Tyr Gly Asp Ala Val Tyr Pro
 385 390 395 400
 Gly Val Val Gly Lys Ser Ala Ile Gly Glu Thr Ser Tyr Arg Gly Phe
 405 410 415
 Tyr Arg Ala Tyr Gln Ala His Val Ser Ser Ser Asn Trp Ala Glu Phe
 420 425 430
 Glu His Ala Ser Ser Thr Trp His Thr Glu Leu Thr Lys Thr Thr Asp
 435 440 445
 Arg

<210> 15
 <211> 449
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> A polypeptide encoded by SEQ ID NO:4.

<400> 15
 Met Asn Tyr Asn Asn Lys Ile Leu Val Ser Glu Ser Gly Leu Ser Gln
 1 5 10 15
 Lys His Leu Ile His Gly Asp Glu Glu Leu Phe Gln His Glu Leu Lys
 20 25 30
 Thr Ile Phe Ala Arg Asn Trp Leu Phe Leu Thr His Asp Ser Leu Ile
 35 40 45
 Pro Ala Pro Gly Asp Tyr Val Thr Ala Lys Met Gly Ile Asp Glu Val
 50 55 60
 Ile Val Ser Arg Gln Asn Asp Gly Ser Ile Arg Ala Phe Leu Asn Val
 65 70 75 80
 Cys Arg His Arg Gly Lys Thr Leu Val Ser Val Glu Ala Gly Asn Ala
 85 90 95
 Lys Gly Phe Val Cys Ser Tyr His Gly Trp Gly Phe Gly Ser Asn Gly
 100 105 110

Glu Leu Gln Ser Val Pro Phe Glu Lys Asp Leu Tyr Gly Glu Ser Leu
 115 120 125
 Asn Lys Lys Cys Leu Gly Leu Lys Glu Val Ala Arg Val Glu Ser Phe
 130 135 140
 His Gly Phe Ile Tyr Gly Cys Phe Asp Gln Glu Ala Pro Pro Leu Met
 145 150 155 160
 Asp Tyr Leu Gly Asp Ala Ala Trp Tyr Leu Glu Pro Met Phe Lys His
 165 170 175
 Ser Gly Gly Leu Glu Leu Val Gly Pro Pro Gly Lys Val Val Ile Lys
 180 185 190
 Ala Asn Trp Lys Ala Pro Ala Glu Asn Phe Val Gly Asp Ala Tyr His
 195 200 205
 Val Gly Trp Thr His Ala Ser Ser Leu Arg Ser Gly Glu Ser Ile Phe
 210 215 220
 Ser Ser Leu Ala Gly Asn Ala Ala Leu Pro Pro Glu Gly Ala Gly Leu
 225 230 235 240
 Gln Met Thr Ser Lys Tyr Gly Ser Gly Met Gly Val Leu Trp Asp Gly
 245 250 255
 Tyr Ser Gly Val His Ser Ala Asp Leu Val Pro Glu Leu Met Ala Phe
 260 265 270
 Gly Gly Ala Lys Gln Glu Arg Leu Asn Lys Glu Ile Gly Asp Val Arg
 275 280 285
 Ala Arg Ile Tyr Arg Ser His Leu Asn Cys Thr Val Phe Pro Asn Asn
 290 295 300
 Ser Met Leu Thr Cys Ser Gly Val Phe Lys Val Trp Asn Pro Ile Asp
 305 310 315 320
 Ala Asn Thr Thr Glu Val Trp Thr Tyr Ala Ile Val Glu Lys Asp Met
 325 330 335
 Pro Glu Asp Leu Lys Arg Arg Leu Ala Asp Ser Val Gln Arg Thr Val
 340 345 350
 Gly Pro Ala Gly Phe Trp Glu Ser Asp Asp Asn Asp Asn Met Glu Thr
 355 360 365
 Ala Ser Gln Asn Gly Lys Lys Tyr Gln Ser Arg Asp Ser Asp Leu Leu
 370 375 380
 Ser Asn Leu Gly Phe Gly Glu Asp Val Tyr Gly Asp Ala Val Tyr Pro
 385 390 395 400
 Gly Val Val Gly Lys Ser Ala Ile Gly Glu Thr Ser Tyr Arg Gly Phe
 405 410 415
 Tyr Arg Ala Tyr Gln Ala His Val Ser Ser Ser Asn Trp Ala Glu Phe
 420 425 430
 Glu His Ala Ser Ser Thr Trp His Thr Glu Leu Thr Lys Thr Thr Asp
 435 440 445
 Arg

<210> 16
 <211> 449
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> A polypeptide encoded by SEQ ID NO:5.

<400> 16
 Met Asn Tyr Asn Asn Lys Ile Leu Val Ser Glu Ser Gly Leu Ser Gln
 1 5 10 15
 Lys His Leu Ile His Gly Asp Glu Glu Leu Phe Gln His Glu Leu Lys
 20 25 30
 Thr Ile Phe Ala Arg Asn Trp Leu Phe Leu Thr His Asp Ser Leu Ile
 35 40 45
 Pro Ala Pro Gly Asp Tyr Val Thr Ala Lys Met Gly Ile Asp Glu Val
 50 55 60

Ile Val Ser Arg Gln Asn Asp Gly Ser Ile Arg Ala Phe Leu Asn Val
 65 70 75 80
 Cys Arg His Arg Gly Lys Thr Leu Val Ser Val Glu Ala Gly Asn Ala
 85 90 95
 Lys Gly Phe Val Cys Ser Tyr His Gly Trp Gly Phe Gly Ser Asn Gly
 100 105 110
 Glu Leu Gln Ser Val Pro Phe Glu Lys Asp Leu Tyr Gly Glu Ser Leu
 115 120 125
 Asn Lys Cys Leu Gly Leu Lys Glu Val Ala Arg Val Glu Ser Phe
 130 135 140
 His Gly Phe Ile Tyr Gly Cys Phe Asp Gln Glu Ala Pro Pro Leu Met
 145 150 155 160
 Asp Tyr Leu Gly Asp Ala Ala Trp Tyr Leu Glu Pro Met Phe Lys His
 165 170 175
 Ser Gly Gly Leu Glu Leu Val Gly Pro Pro Gly Lys Val Val Ile Lys
 180 185 190
 Ala Asn Trp Lys Ala Pro Ala Glu Asn Phe Val Gly Asp Ala Tyr His
 195 200 205
 Val Gly Trp Thr His Ala Ser Ser Leu Arg Ser Gly Glu Ser Ile Phe
 210 215 220
 Cys Ser Leu Ala Gly Asn Ala Ala Leu Pro Pro Glu Gly Ala Gly Leu
 225 230 235 240
 Gln Met Thr Ser Lys Tyr Gly Ser Gly Met Gly Val Leu Trp Asp Gly
 245 250 255
 Tyr Ser Gly Val His Ser Ala Asp Leu Val Pro Glu Leu Met Ala Phe
 260 265 270
 Gly Gly Ala Lys Gln Glu Arg Leu Asn Lys Glu Ile Gly Asp Val Arg
 275 280 285
 Ala Arg Ile Tyr Arg Ser His Leu Asn Cys Thr Val Phe Pro Asn Asn
 290 295 300
 Ser Met Leu Thr Cys Ser Gly Val Phe Lys Val Trp Asn Pro Ile Asp
 305 310 315 320
 Ala Asn Thr Thr Glu Val Trp Thr Tyr Ala Ile Val Glu Lys Asp Met
 325 330 335
 Pro Glu Asp Leu Lys Arg Arg Leu Ala Asp Ser Val Gln Arg Thr Val
 340 345 350
 Gly Pro Ala Gly Phe Trp Glu Ser Asp Asp Asn Asn Met Glu Thr
 355 360 365
 Ala Ser Gln Asn Gly Lys Tyr Gln Ser Arg Asp Ser Asp Leu Leu
 370 375 380
 Ser Asn Leu Gly Phe Gly Glu Asp Val Tyr Gly Asp Ala Val Tyr Pro
 385 390 395 400
 Gly Val Val Gly Lys Ser Ala Ile Gly Glu Thr Ser Tyr Arg Gly Phe
 405 410 415
 Tyr Arg Ala Tyr Gln Ala His Val Ser Ser Ser Asn Trp Ala Glu Phe
 420 425 430
 Glu His Ala Ser Ser Thr Trp His Thr Glu Leu Thr Lys Thr Thr Asp
 435 440 445
 Arg

<210> 17
 <211> 449
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> A polypeptide encoded by SEQ ID NO:6.

<400> 17
 Met Asn Tyr Asn Asn Lys Ile Leu Val Ser Glu Phe Gly Leu Ser Gln
 1 5 10 15

Lys His Leu Ile His Gly Asp Glu Glu Leu Phe Gln His Glu Leu Lys
 20 25 30
 Thr Ile Phe Ala Arg Asn Trp Leu Phe Leu Thr His Asp Ser Leu Ile
 35 40 45
 Pro Ala Pro Gly Asp Tyr Val Thr Ala Lys Met Gly Ile Asp Glu Val
 50 55 60
 Ile Val Ser Arg Gln Asn Asp Gly Ser Ile Arg Ala Phe Leu Asn Val
 65 70 75 80
 Cys Arg His Arg Gly Lys Thr Leu Val Ser Val Glu Ala Gly Asn Ala
 85 90 95
 Lys Gly Phe Val Cys Ser Tyr His Gly Trp Gly Phe Gly Ser Asn Gly
 100 105 110
 Glu Leu Gln Ser Val Pro Phe Glu Lys Asp Leu Tyr Gly Glu Ser Leu
 115 120 125
 Asn Lys Lys Cys Leu Gly Leu Lys Glu Val Ala Arg Val Glu Ser Phe
 130 135 140
 His Gly Phe Ile Tyr Gly Cys Phe Asp Gln Glu Ala Pro Pro Leu Met
 145 150 155 160
 Asp Tyr Leu Gly Asp Ala Ala Trp Tyr Leu Glu Pro Met Phe Lys His
 165 170 175
 Ser Gly Gly Leu Glu Leu Val Gly Pro Pro Gly Lys Val Val Ile Lys
 180 185 190
 Ala Asn Trp Lys Ala Pro Ala Glu Asn Phe Val Gly Asp Ala Tyr His
 195 200 205
 Val Gly Trp Thr His Ala Ser Ser Leu Arg Ser Gly Glu Ser Ile Phe
 210 215 220
 Ser Ser Leu Ala Gly Asn Ala Ala Leu Pro Pro Glu Gly Ala Gly Leu
 225 230 235 240
 Gln Met Thr Ser Lys Tyr Gly Ser Gly Met Gly Val Leu Trp Asp Gly
 245 250 255
 Tyr Ser Gly Val His Ser Ala Asp Leu Val Pro Glu Leu Met Ala Phe
 260 265 270
 Gly Gly Ala Lys Gln Glu Arg Leu Asn Lys Glu Ile Gly Asp Val Arg
 275 280 285
 Ala Arg Ile Tyr Arg Ser His Leu Asn Cys Thr Val Phe Pro Asn Asn
 290 295 300
 Ser Met Leu Thr Cys Ser Gly Val Phe Lys Val Trp Asn Pro Ile Asp
 305 310 315 320
 Ala Asn Thr Thr Glu Val Trp Thr Tyr Ala Ile Val Glu Lys Asp Met
 325 330 335
 Pro Glu Asp Leu Lys Arg Arg Leu Ala Asp Ser Val Gln Arg Thr Val
 340 345 350
 Gly Pro Ala Gly Phe Trp Glu Ser Asp Asp Asn Asn Met Glu Thr
 355 360 365
 Ala Ser Gln Asn Gly Lys Lys Tyr Gln Ser Arg Asp Ser Asp Leu Leu
 370 375 380
 Ser Asn Leu Gly Phe Gly Glu Asp Val Tyr Gly Asp Ala Val Tyr Pro
 385 390 395 400
 Gly Val Val Gly Lys Ser Ala Ile Gly Glu Thr Ser Tyr Arg Gly Phe
 405 410 415
 Tyr Arg Ala Tyr Arg Ala His Val Ser Ser Ser Asn Trp Ala Glu Phe
 420 425 430
 Glu His Ala Ser Ser Thr Trp His Thr Glu Leu Thr Lys Thr Thr Asp
 435 440 445
 Arg

<210> 18
 <211> 449
 <212> PRT
 <213> Artificial Sequence

<220>

<223> A polypeptide encoded by SEQ ID NO:7.

<400> 18

Met Asn Tyr Lys Asn Lys Ile Leu Val Ser Glu Ser Gly Leu Thr Gln
 1 5 10 15
 Lys His Leu Ile His Gly Asp Glu Glu Leu Phe Gln His Glu Leu Arg
 20 25 30
 Thr Ile Phe Ala Arg Asn Trp Leu Phe Leu Thr His Asp Ser Leu Ile
 35 40 45
 Pro Ser Pro Gly Asp Tyr Val Thr Ala Lys Met Gly Ile Asp Glu Val
 50 55 60
 Ile Val Ser Arg Gln Ser Asp Gly Ser Ile Arg Ala Phe Leu Asn Val
 65 70 75 80
 Cys Arg His Arg Gly Lys Thr Leu Val Asn Ala Glu Ala Gly Asn Ala
 85 90 95
 Lys Gly Phe Val Cys Ser Tyr His Gly Trp Gly Phe Gly Ser Asn Gly
 100 105 110
 Glu Leu Gln Ser Val Pro Phe Glu Lys Glu Leu Tyr Gly Glu Ser Leu
 115 120 125
 Asn Lys Lys Cys Leu Gly Leu Lys Glu Val Ala Arg Val Glu Ser Phe
 130 135 140
 His Gly Phe Ile Tyr Gly Cys Phe Asp Gln Glu Ala Pro Pro Leu Met
 145 150 155 160
 Asp Tyr Leu Gly Asp Ala Ala Trp Tyr Leu Glu Pro Ile Phe Lys His
 165 170 175
 Ser Gly Gly Leu Glu Leu Val Gly Pro Pro Gly Lys Val Val Ile Lys
 180 185 190
 Ala Asn Trp Lys Ala Pro Ala Glu Asn Phe Val Gly Asp Ala Tyr His
 195 200 205
 Val Gly Trp Thr His Ala Ser Ser Leu Arg Ser Gly Glu Ser Ile Phe
 210 215 220
 Ala Ser Leu Ala Gly Asn Ala Val Leu Pro Pro Glu Gly Ala Gly Leu
 225 230 235 240
 Gln Met Thr Ser Lys Tyr Gly Ser Gly Met Gly Val Leu Trp Asp Gly
 245 250 255
 Tyr Ser Gly Val His Ser Ala Asp Leu Val Pro Glu Leu Met Ala Phe
 260 265 270
 Gly Gly Ser Lys Gln Glu Arg Leu Asn Lys Glu Ile Gly Asp Val Arg
 275 280 285
 Ala Arg Ile Tyr Arg Ser His Leu Asn Cys Thr Val Phe Pro Asn Asn
 290 295 300
 Ser Met Leu Thr Cys Ser Gly Val Phe Lys Val Trp Asn Pro Ile Asp
 305 310 315 320
 Ala Asn Thr Thr Glu Val Trp Thr Tyr Ala Ile Val Glu Lys Asp Met
 325 330 335
 Pro Glu Asp Leu Lys Arg Arg Leu Ala Asp Ser Val Gln Arg Thr Val
 340 345 350
 Gly Pro Ala Gly Phe Trp Glu Ser Asp Asp Asn Asn Met Glu Thr
 355 360 365
 Ala Ser Gln Asn Gly Lys Lys Tyr Gln Ser Arg Asp Ser Asp Leu Leu
 370 375 380
 Ser Asn Leu Gly Phe Gly Lys Asp Val Tyr Gly Asp Ala Val Tyr Pro
 385 390 395 400
 Gly Val Val Gly Lys Ser Ala Ile Gly Glu Thr Ser Tyr Arg Gly Phe
 405 410 415
 Tyr Arg Ala Tyr Gln Ala His Val Ser Ser Asn Trp Ala Glu Phe
 420 425 430
 Glu Asp Ala Ser Ser Thr Trp His Thr Glu Leu Thr Lys Thr Thr Asp
 435 440 445
 Arg

<210> 19
 <211> 449
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> A polypeptide encoded by SEQ ID NO:8.

<221> SITE
 <222> (35)...(35)
 <223> Xaa = any amino acid.

<400> 19
 Met Asn Tyr Lys Asn Lys Ile Leu Val Ser Glu Ser Gly Leu Thr Gln
 1 5 10 15
 Lys His Leu Ile His Gly Asp Glu Glu Leu Phe Gln His Glu Leu Arg
 20 25 30
 Thr Ile Xaa Ala Arg Asn Trp Leu Phe Leu Thr His Asp Ser Leu Ile
 35 40 45
 Pro Ser Pro Gly Asp Tyr Val Thr Ala Lys Met Gly Ile Asp Glu Val
 50 55 60
 Ile Val Ser Arg Gln Ser Asp Gly Ser Ile Arg Ala Phe Leu Asn Val
 65 70 75 80
 Cys Arg His Arg Gly Lys Thr Leu Val Asn Ala Glu Ala Gly Asn Ala
 85 90 95
 Lys Gly Phe Val Cys Ser Tyr His Gly Trp Gly Phe Gly Ser Asn Gly
 100 105 110
 Glu Leu Gln Ser Val Pro Phe Glu Lys Glu Leu Tyr Gly Glu Ser Leu
 115 120 125
 Asn Lys Lys Cys Leu Gly Leu Lys Glu Val Ala Arg Val Glu Ser Phe
 130 135 140
 His Gly Phe Ile Tyr Gly Cys Phe Asp Gln Glu Ala Pro Ser Leu Met
 145 150 155 160
 Asp Tyr Leu Gly Asp Ala Ala Trp Tyr Leu Glu Pro Ile Phe Lys His
 165 170 175
 Ser Gly Gly Leu Glu Leu Val Gly Pro Pro Gly Lys Val Val Ile Lys
 180 185 190
 Ala Asn Trp Lys Ala Pro Ala Glu Asn Phe Val Gly Asp Ala Tyr His
 195 200 205
 Val Gly Trp Thr His Ala Ser Ser Leu Arg Thr Gly Glu Ser Ile Phe
 210 215 220
 Ser Ser Leu Ala Gly Asn Ala Val Leu Pro Pro Glu Gly Ala Gly Leu
 225 230 235 240
 Gln Met Thr Ser Lys Tyr Gly Ser Gly Met Gly Val Leu Trp Asp Gly
 245 250 255
 Tyr Ser Gly Val His Ser Ala Asp Leu Val Pro Glu Leu Met Ala Phe
 260 265 270
 Gly Gly Ala Lys Gln Glu Arg Leu Asn Lys Glu Ile Gly Asp Val Pro
 275 280 285
 Ala Arg Ile Tyr Arg Ser His Leu Asn Cys Thr Val Phe Pro Asn Asn
 290 295 300
 Ser Val Leu Thr Cys Ser Gly Val Phe Lys Val Trp Asn Pro Ile Asp
 305 310 315 320
 Ala Asn Thr Thr Glu Val Trp Thr Tyr Ala Ile Val Glu Lys Asp Met
 325 330 335
 Pro Glu Asp Leu Lys Arg Arg Leu Ala Asp Ala Val Gln Arg Thr Val
 340 345 350
 Gly Pro Ala Gly Phe Trp Glu Ser Asp Asp Asn Asp Asn Met Glu Thr
 355 360 365
 Ala Ser Gln Asn Gly Lys Lys Tyr Gln Ser Arg Asp Ser Asp Leu Ile
 370 375 380

Ser Asn Leu Gly Phe Gly Lys Asp Val Tyr Gly Asp Ala Val Tyr Pro
 385 390 395 400
 Gly Val Val Gly Lys Ser Ala Ile Gly Glu Thr Ser Tyr Arg Gly Phe
 405 410 415
 Tyr Arg Ala Tyr Gln Ala His Val Ser Ser Ser Asn Trp Ala Glu Phe
 420 425 430
 Glu Asp Ala Ser Ser Thr Trp His Thr Glu Leu Thr Lys Thr Thr Asp
 435 440 445
 Arg

<210> 20
 <211> 449
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> A polypeptide encoded by SEQ ID NO:9.

<400> 20
 Met Asn Tyr Lys Asn Lys Ile Leu Val Ser Glu Ser Gly Leu Thr Gln
 1 5 10 15
 Lys His Leu Ile His Gly Gly Glu Gly Leu Phe Gln His Glu Leu Arg
 20 25 30
 Ala Val Phe Ala Arg Asn Trp Leu Phe Leu Thr His Asp Ser Leu Ile
 35 40 45
 Pro Ser Pro Gly Asp Tyr Val Thr Ala Lys Met Gly Ile Asp Glu Val
 50 55 60
 Ile Val Ser Arg Gln Ser Asp Gly Ser Ile Arg Ala Phe Leu Asn Val
 65 70 75 80
 Cys Arg His Arg Gly Lys Thr Leu Val Asn Ala Glu Ala Gly Asn Ala
 85 90 95
 Lys Gly Phe Val Cys Ser Tyr His Gly Trp Gly Phe Gly Ser Asn Gly
 100 105 110
 Glu Leu Gln Ser Val Pro Phe Glu Lys Glu Leu Tyr Gly Glu Ser Leu
 115 120 125
 Asn Lys Lys Cys Leu Gly Leu Lys Glu Val Ala Arg Val Glu Ser Phe
 130 135 140
 His Gly Phe Ile Tyr Ala Cys Ile Asp Gln Glu Ala Pro Ser Leu Met
 145 150 155 160
 Asp Tyr Leu Gly Asp Ala Ala Trp Tyr Leu Glu Pro Ile Phe Lys His
 165 170 175
 Ser Gly Gly Leu Glu Leu Val Gly Pro Pro Gly Lys Val Val Ile Lys
 180 185 190
 Ala Asn Trp Lys Ala Pro Ala Glu Asn Phe Val Gly Asp Ala Tyr His
 195 200 205
 Val Gly Trp Thr His Ala Ser Ser Leu Cys Thr Gly Glu Ser Ile Phe
 210 215 220
 Ser Ser Leu Ala Gly Asn Ala Val Leu Pro Pro Glu Gly Ala Gly Leu
 225 230 235 240
 Gln Met Thr Ser Lys Tyr Gly Ser Gly Met Gly Val Leu Trp Asp Gly
 245 250 255
 Tyr Ser Gly Val His Ser Ala Asp Leu Val Pro Glu Leu Met Ala Phe
 260 265 270
 Gly Gly Ala Lys Gln Glu Arg Leu Asn Lys Glu Ile Gly Asp Val Arg
 275 280 285
 Ala Arg Ile Tyr Arg Ser His Leu Asn Cys Thr Val Phe Pro Asn Asn
 290 295 300
 Ser Val Leu Thr Cys Ser Gly Val Phe Lys Val Trp Asn Pro Ile Asp
 305 310 315 320
 Ala Asn Thr Thr Glu Val Trp Thr Tyr Ala Ile Val Glu Lys Asp Met
 325 330 335

Pro Glu Asp Leu Lys Arg Arg Leu Ala Asp Ala Val Gln Arg Thr Val
 340 345 350
 Gly Pro Ala Gly Phe Trp Glu Ser Asp Asp Asn Asn Met Glu Thr
 355 360 365
 Ala Ser Gln Asn Gly Lys Lys Tyr Gln Ser Arg Asp Ser Asp Leu Ile
 370 375 380
 Ser Asn Leu Gly Phe Gly Lys Asp Val Tyr Gly Asp Ala Val Tyr Pro
 385 390 395 400
 Gly Val Val Gly Lys Ser Ala Ile Gly Glu Thr Ser Tyr Arg Gly Phe
 405 410 415
 Tyr Arg Ala Tyr Gln Ala His Val Ser Ser Ser Asn Trp Ala Glu Phe
 420 425 430
 Glu Asp Ala Ser Ser Thr Trp His Thr Glu Leu Thr Lys Thr Thr Asp
 435 440 445
 Arg

<210> 21
 <211> 449
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> A polypeptide encoded by SEQ ID NO:10.

<400> 21
 Met Asn Tyr Lys Asn Lys Asn Leu Val Ser Glu Ser Gly Leu Thr Gln
 1 5 10 15
 Lys His Leu Ile His Gly Asp Glu Glu Leu Phe Gln Arg Glu Leu Glu
 20 25 30
 Thr Ile Phe Ala Arg Asn Trp Leu Phe Leu Thr His Asp Ser Leu Ile
 35 40 45
 Pro Ser Pro Gly Asp Tyr Val Thr Ala Lys Met Gly Val Asp Glu Val
 50 55 60
 Ile Val Ser Arg Gln Asn Asp Gly Ser Ile Arg Ala Phe Leu Asn Val
 65 70 75 80
 Cys Arg His Arg Gly Lys Thr Leu Val His Ala Glu Ala Gly Asn Ala
 85 90 95
 Lys Gly Phe Val Cys Ser Tyr His Gly Trp Gly Phe Gly Ala Asn Gly
 100 105 110
 Glu Leu Gln Ser Val Pro Phe Glu Lys Glu Leu Tyr Gly Glu Ala Leu
 115 120 125
 Asp Lys Lys Cys Met Gly Leu Lys Glu Val Ala Arg Val Glu Ser Phe
 130 135 140
 His Gly Phe Ile Tyr Gly Cys Phe Asp Glu Glu Ala Pro Ser Leu Lys
 145 150 155 160
 Asp Tyr Met Gly Asp Ala Gly Trp Tyr Leu Glu Pro Met Phe Lys His
 165 170 175
 Ser Gly Gly Leu Glu Leu Ile Gly Pro Pro Gly Lys Val Ile Ile Lys
 180 185 190
 Ala Asn Trp Lys Ala Pro Ala Glu Asn Phe Thr Gly Asp Ala Tyr His
 195 200 205
 Val Gly Trp Thr His Ala Ser Ser Leu Arg Ser Gly Gln Ser Val Phe
 210 215 220
 Ser Ser Leu Ala Gly Asn Ala Ala Leu Pro Pro Glu Gly Ala Gly Leu
 225 230 235 240
 Gln Met Thr Ser Lys Tyr Gly Ser Gly Met Gly Val Leu Trp Asp Gly
 245 250 255
 Tyr Ser Gly Val His Ser Ala Asp Leu Val Pro Glu Leu Met Ala Phe
 260 265 270
 Gly Gly Ala Lys Gln Glu Arg Leu Asn Lys Glu Ile Gly Glu Val Arg
 275 280 285

Ala Arg Ile Tyr Arg Ser His Leu Asn Cys Thr Val Phe Pro Asn Asn
 290 295 300
 Ser Phe Leu Thr Cys Ser Gly Val Phe Lys Val Trp His Pro Ile Asp
 305 310 315 320
 Ala Asn Thr Thr Glu Val Trp Thr Tyr Ala Met Val Glu Lys Asp Met
 325 330 335
 Pro Glu Asp Leu Lys Arg Arg Leu Val Asp Ala Val Gln Arg Thr Val
 340 345 350
 Gly Pro Ala Gly Phe Trp Glu Ser Asp Asp Asn Asn Met Glu Thr
 355 360 365
 Val Ser Gln Asn Ala Lys Lys Tyr Gln Ser Arg Asp Gly Asp Leu Val
 370 375 380
 Ser Asn Leu Gly Phe Gly Gly Asp Val Tyr Gly Asp Glu Val Tyr Pro
 385 390 395 400
 Gly Ile Val Gly Lys Ser Ala Ile Gly Glu Thr Ser Tyr Arg Gly Phe
 405 410 415
 Tyr Arg Ala Tyr Gly Ala His Ile Ser Ser Ser Trp Ala Glu Phe
 420 425 430
 Glu Asp Val Ser Lys Asn Trp His Thr Glu Leu Ala Lys Thr Thr Asp
 435 440 445
 Arg

<210> 22
 <211> 447
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> A polypeptide encoded by SEQ ID NO:11.

<400> 22
 Met Ile Tyr Glu Asn Leu Val Ser Glu Ala Gly Leu Thr Gln Lys His
 1 5 10 15
 Leu Ile His Gly Asp Lys Glu Leu Phe Gln His Glu Leu Lys Thr Ile
 20 25 30
 Phe Ala Arg Asn Trp Leu Phe Leu Thr His Asp Ser Leu Ile Pro Ser
 35 40 45
 Pro Gly Asp Tyr Val Thr Ala Lys Met Gly Val Asp Glu Val Ile Val
 50 55 60
 Ser Arg Gln Asn Asp Gly Ser Val Arg Ala Phe Leu Asn Val Cys Arg
 65 70 75 80
 His Arg Gly Lys Thr Leu Val His Ala Glu Ala Gly Asn Ala Lys Gly
 85 90 95
 Phe Val Cys Ser Tyr His Gly Trp Gly Phe Gly Ser Asn Gly Glu Leu
 100 105 110
 Gln Ser Val Pro Phe Glu Lys Glu Leu Tyr Gly Asp Thr Ile Lys Lys
 115 120 125
 Lys Cys Leu Gly Leu Lys Glu Val Pro Arg Ile Glu Ser Phe His Gly
 130 135 140
 Phe Ile Tyr Gly Cys Phe Asp Ala Glu Ala Pro Thr Leu Val Asp Tyr
 145 150 155 160
 Leu Gly Asp Ala Ala Trp Tyr Leu Glu Pro Ile Phe Lys His Ser Gly
 165 170 175
 Gly Leu Glu Leu Val Gly Pro Pro Gly Lys Val Val Ile Lys Ala Asn
 180 185 190
 Trp Lys Ala Pro Ala Glu Asn Phe Val Gly Asp Ala Tyr His Val Gly
 195 200 205
 Trp Thr His Ala Ser Ser Leu Arg Ser Gly Gln Ser Ile Phe Thr Pro
 210 215 220
 Leu Ala Gly Asn Ala Met Leu Pro Pro Glu Gly Ala Gly Leu Gln Met
 225 230 235 240

Thr Ser Lys Tyr Gly Ser Gly Met Gly Val Leu Trp Asp Gly Tyr Ser
 245 250 255
 Gly Val His Ser Ala Asp Leu Val Pro Glu Met Met Ala Phe Gly Gly
 260 265 270
 Ala Lys Gln Glu Lys Leu Ala Lys Glu Ile Gly Asp Val Arg Ala Arg
 275 280 285
 Ile Tyr Arg Ser His Leu Asn Cys Thr Val Phe Pro Asn Asn Ser Ile
 290 295 300
 Leu Thr Cys Ser Gly Val Phe Lys Val Trp Asn Pro Ile Asp Glu Asn
 305 310 315 320
 Thr Thr Glu Val Trp Thr Tyr Ala Ile Val Glu Lys Asp Met Pro Glu
 325 330 335
 Asp Leu Lys Arg Arg Leu Ala Asp Ala Val Gln Arg Thr Val Gly Pro
 340 345 350
 Ala Gly Phe Trp Glu Ser Asp Asp Asn Asp Asn Met Glu Thr Glu Ser
 355 360 365
 Gln Asn Ala Lys Lys Tyr Gln Ser Ser Asn Ser Asp Leu Ile Ala Asn
 370 375 380
 Leu Gly Phe Gly Lys Asp Val Tyr Gly Asp Glu Cys Tyr Pro Gly Val
 385 390 395 400
 Val Ala Lys Ser Ala Ile Gly Glu Thr Ser Tyr Arg Gly Phe Tyr Arg
 405 410 415
 Ala Tyr Gln Ala His Ile Ser Ser Asn Trp Ala Glu Phe Glu Asn
 420 425 430
 Thr Ser Arg Asn Trp His Thr Glu Leu Thr Lys Thr Thr Asp Arg
 435 440 445

<210> 23

<211> 447

<212> PRT

<213> Artificial Sequence

<220>

<223> A polypeptide encoded by SEQ ID NO:12.

<400> 23

Met Ser Tyr Gln Asn Leu Val Ser Glu Ala Gly Leu Thr Gln Lys Leu
 1 5 10 15
 Leu Ile His Gly Asp Lys Glu Leu Phe Gln His Glu Leu Lys Thr Ile
 20 25 30
 Phe Ala Arg Asn Trp Leu Phe Leu Thr His Asp Ser Leu Ile Pro Ser
 35 40 45
 Pro Gly Asp Tyr Val Thr Ala Lys Met Gly Val Asp Glu Val Ile Val
 50 55 60
 Ser Arg Gln Asn Asp Gly Ser Val Arg Ala Phe Leu Asn Val Cys Arg
 65 70 75 80
 His Arg Gly Lys Thr Leu Val His Thr Glu Ala Gly Asn Ala Lys Gly
 85 90 95
 Phe Val Cys Gly Tyr His Gly Trp Gly Tyr Gly Ser Asn Gly Glu Leu
 100 105 110
 Gln Ser Val Pro Phe Glu Lys Glu Leu Tyr Gly Asp Ala Ile Lys Lys
 115 120 125
 Lys Cys Leu Gly Leu Lys Glu Val Pro Arg Ile Glu Ser Phe His Gly
 130 135 140
 Phe Ile Tyr Gly Cys Phe Asp Ala Glu Ala Pro Pro Leu Ile Asp Tyr
 145 150 155 160
 Leu Gly Asp Ala Ala Trp Tyr Leu Glu Pro Thr Phe Lys His Ser Gly
 165 170 175
 Gly Leu Glu Leu Val Gly Pro Pro Gly Lys Val Val Val Lys Ala Asn
 180 185 190
 Trp Lys Pro Phe Ala Glu Asn Phe Val Gly Asp Ile Tyr His Val Gly
 195 200 205

Trp Thr His Ala Ala Ala Leu Arg Ala Gly Gln Ser Val Phe Ser Ser
 210 215 220
 Leu Ala Gly Asn Ala Lys Leu Pro Pro Glu Gly Ala Gly Leu Gln Met
 225 230 235 240
 Thr Ser Lys Tyr Gly Ser Gly Met Gly Leu Thr Trp Asp Tyr Tyr Ser
 245 250 255
 Gly Asn Phe Ser Ala Asp Met Val Pro Asp Leu Met Ala Phe Gly Ala
 260 265 270
 Ala Lys Gln Glu Lys Leu Ala Lys Glu Ile Gly Asp Val Arg Ala Arg
 275 280 285
 Ile Tyr Arg Ser Ile Leu Asn Gly Thr Val Phe Pro Asn Asn Ser Phe
 290 295 300
 Leu Thr Gly Ser Ala Thr Phe Lys Val Trp Asn Pro Ile Asp Glu Asn
 305 310 315 320
 Thr Thr Glu Val Trp Thr Tyr Ala Phe Val Glu Lys Asp Met Pro Glu
 325 330 335
 Asp Leu Lys Arg Arg Leu Ala Asp Ala Ala Gln Arg Ser Val Gly Pro
 340 345 350
 Ala Gly Phe Trp Glu Ser Asp Asp Asn Glu Asn Met Glu Thr Leu Ser
 355 360 365
 Gln Asn Ala Lys Lys Tyr Gln Ser Ser Asn Ser Asp Gln Ile Ala Ser
 370 375 380
 Leu Gly Phe Gly Lys Asp Val Tyr Gly Asp Glu Cys Tyr Pro Gly Val
 385 390 395 400
 Val Gly Lys Ser Ala Ile Gly Glu Thr Ser Tyr Arg Gly Phe Tyr Arg
 405 410 415
 Ala Tyr Gln Ala His Ile Ser Ser Asn Trp Ala Glu Phe Glu Asn
 420 425 430
 Ala Ser Arg Asn Trp His Thr Glu Leu Thr Lys Thr Thr Asp Arg
 435 440 445

<210> 24
 <211> 451
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> A polypeptide encoded by SEQ ID NO:13.

<400> 24

Met Arg Gln Ala Ile Met Ser Tyr Gln Asn Leu Val Ser Glu Ala Gly
 1 5 10 15
 Leu Thr Gln Lys His Leu Ile Tyr Gly Asp Lys Glu Leu Phe Gln His
 20 25 30
 Glu Leu Lys Thr Ile Phe Ala Arg Asn Trp Leu Phe Leu Thr His Asp
 35 40 45
 Ser Leu Ile Pro Ser Pro Gly Asp Tyr Val Lys Ala Lys Met Gly Val
 50 55 60
 Asp Glu Val Ile Val Ser Arg Gln Asn Asp Gly Ser Val Arg Ala Phe
 65 70 75 80
 Leu Asn Val Cys Arg His Arg Gly Lys Thr Ile Val Asp Ala Glu Ala
 85 90 95
 Gly Asn Ala Lys Gly Phe Val Cys Gly Tyr His Gly Trp Gly Tyr Gly
 100 105 110
 Ser Asn Gly Glu Leu Gln Ser Val Pro Phe Glu Lys Glu Leu Tyr Gly
 115 120 125
 Asp Ala Ile Lys Lys Cys Leu Gly Leu Lys Glu Val Pro Arg Ile
 130 135 140
 Glu Ser Phe His Gly Phe Ile Tyr Gly Cys Phe Asp Ala Glu Ala Pro
 145 150 155 160
 Pro Leu Ile Asp Tyr Leu Gly Asp Val Ala Trp Tyr Leu Glu Pro Thr
 165 170 175

Phe Lys His Ser Gly Gly Leu Glu Leu Val Gly Pro Pro Ala Lys Val
 180 185 190
 Val Val Lys Gly Asn Trp Lys Val Phe Ala Glu Asn Phe Val Gly Asp
 195 200 205
 Ile Tyr His Ile Gly Trp Thr His Ala Ser Ile Leu Arg Ala Gly Gln
 210 215 220
 Ala Ile Phe Ala Pro Leu Ala Gly Asn Ala Met Leu Pro Pro Glu Gly
 225 230 235 240
 Thr Gly Leu Gln Ala Thr Thr Lys Tyr Gly Ser Gly Ile Gly Val Ser
 245 250 255
 Leu Asp Ala Tyr Ser Gly Val Gln Ser Ala Asp Leu Val Pro Glu Met
 260 265 270
 Met Ala Phe Gly Gly Ala Lys Gln Glu Lys Leu Ala Lys Glu Ile Gly
 275 280 285
 Asp Val Arg Ala Arg Ile Tyr Arg Ser Gln Val Asn Gly Thr Val Phe
 290 295 300
 Pro Asn Asn Cys Phe Leu Thr Gly Ala Gly Val Phe Lys Val Phe Asn
 305 310 315 320
 Pro Ile Asp Glu Asn Thr Thr Glu Ala Trp Thr Tyr Ala Ile Val Glu
 325 330 335
 Lys Asp Met Pro Glu Asp Leu Lys Arg Arg Leu Ala Asp Ala Ala Gln
 340 345 350
 Arg Ser Val Gly Pro Ala Gly Tyr Trp Glu Ser Asp Asp Asn Asp Asn
 355 360 365
 Met Val Leu Ser Gln Asn Ala Lys Lys Tyr Gln Ser Ser Asn Ser Asp
 370 375 380
 Leu Ile Ala Asp Leu Gly Phe Gly Lys Asp Val Tyr Gly Asp Glu Cys
 385 390 395 400
 Tyr Pro Gly Val Val Ser Lys Ser Ala Phe Ser Glu Thr Asn His Arg
 405 410 415
 Gly Phe Tyr Arg Ala Tyr Gln Ala His Ile Ser Ser Ser Asn Trp Ala
 420 425 430
 Glu Phe Glu Asn Thr Ser Arg Asn Trp His Thr Glu Leu Thr Lys Thr
 435 440 445
 Thr Asp Arg
 450

<210> 25

<211> 2265

<212> DNA

<213> Pseudomonas sp.

<400> 25

gagggttagag	aaatcgaatg	ccccttgcat	caaggtcgg	ttgacgttg	cacaggcaaa	60
gccctgtgcg	cacccgtgac	acagaacatc	aaaacatatac	cagtcaagat	tgagaacctg	120
cgcgtaatga	ttgattttag	ctaagaattt	taacaggagg	caccccgggc	cctagagcgt	180
aatcaccccc	attccatctt	ttttaggtga	aaacatgaat	tacaataata	aatcttgg	240
aagtgaatct	ggtctgagcc	aaaagcacct	gattcatggc	gatgaagaac	tttccaaca	300
tgaactgaaa	accattttg	cgcggactg	gcttttctc	actcatgata	gcctgattcc	360
tgccccccgc	gactatgtt	ccgcaaaaat	ggggattgac	gaggtcatcg	tctcccgca	420
gaacgacgg	tcgattcgt	cttttctgaa	cggttgcgg	catcgtggca	agacgctgg	480
gagcgtggaa	gccggcaatg	ccaaaggttt	tgtttgcagc	tatcacggct	ggggcttcgg	540
ctccaaacgg	gaactgcaga	gcgttccatt	tgaaaaagat	ctgtacggcg	agtcgctcaa	600
taaaaaatgt	ctggggttga	aagaagtgc	tcgcgtggag	agttccatcg	gcttcatcta	660
cggttgc	gaccaggagg	cccctctct	tatggactat	ctgggtgacg	ctgcttggta	720
cctggAACCT	atgttcaagc	attccggcgg	tttagaactg	gtcggtcctc	caggcaaggt	780
tgtgatcaag	gccaactgga	aggcaccgc	ggaaaacttt	gtgggagatg	cataaccacgt	840
gggttggacg	cacgcgtctt	cgcttcgctc	gggggagttt	atcttctcg	cgctcgctgg	900
caatgcggcg	ctaccacctg	aaggcgcagg	cttgcggaaatg	acctccaaat	acggcagcgg	960
catgggtgtg	ttgtggacg	gatattcagg	tgtgcatacg	gcagacttgg	ttccggaaatt	1020
gatggcattc	ggaggcgcgg	agcaggaaag	gctgaacaaa	gaaattggcg	atgttcgcgc	1080
tcggatttat	cgcagccacc	tcaactgcac	cgttttcccg	aacaacagca	tgctgacctg	1140

ctcgggtgtt	ttcaaaagtat	ggaacccgat	cgacgcaaac	accaccgagg	tctggaccta	1200
cgcattgtc	gaaaaagaca	tgcctgagga	tctcaagcgc	cgcttggcgc	actctgttca	1260
gcgaacgttc	gggcctgctg	gcttctggga	aagcgacgac	aatgacaata	tggaaacagc	1320
ttcgcaaaac	ggcaagaat	atcaatcaag	agatagtat	ctgcttcaa	accttggttt	1380
cggtgaggac	gtatacggcg	acgcccgtcta	tccagggcgtc	gtcggcaat	cgggatcg	1440
cgagaccagt	tatcggtt	tctaccgggc	ttaccaggca	cacgtcagca	gctccaactg	1500
ggctgagttc	gagcatgcct	ctagtacttg	gcatactgaa	cttacgaaga	ctaactgatcg	1560
ctaacagacg	agtgcaccat	gtatcaat	attcaagaag	acaagcttgtt	ttccgcccac	1620
gacgcccgaag	agattcttcg	tttcttcaat	tgccacgact	ctgctttgca	acaagaagcc	1680
actacgctgc	tgacccagga	agcgcatttg	ttggacatttc	aggcttaccg	tgcttggta	1740
gagcaactgctg	tggggttcaga	ggtgcaatata	caggtcattt	cacgcgaact	gcgcgcagct	1800
tcagagcgtc	gttataaagct	caatgaagcc	atgaacgttt	acaacgaaaa	ttttcagcaa	1860
ctgaaaagttc	gagttgagca	tcaactggat	ccgcaaaact	ggggcaacag	cccgaaagctg	1920
cgttttactc	gttttatcac	caacgtccag	gccgcaatgg	acgtaaaatga	caaagagcta	1980
cttcacatcc	gctccaaacgt	cattctgcac	cgggcacgac	gtggcaatca	ggtcgatgtc	2040
ttctacgccc	cccgaaaga	taaatggaaa	cgtggcgaag	gtggagtacg	aaaattggtc	2100
cagcgattcg	tcgattaccc	agagcgcata	ttcagacgc	acaatctgtat	ggtctttctg	2160
tgattcagtg	accattttta	caaatggtc	ctgcaaccgc	ggtcaccatt	aatcaaaggg	2220
aatgtacgtg	tatggcaat	caacaagtgc	tttcgataac	cggtg		2265

<210> 26

<211> 449

<212> PRT

<213> Pseudomonas sp.

<400> 26

Met	Asn	Tyr	Asn	Asn	Lys	Ile	Leu	Val	Ser	Glu	Ser	Gly	Leu	Ser	Gln
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Lys	His	Leu	Ile	His	Gly	Asp	Glu	Glu	Leu	Phe	Gln	His	Glu	Leu	Lys
									20		25		30		
Thr	Ile	Phe	Ala	Arg	Asn	Trp	Leu	Phe	Leu	Thr	His	Asp	Ser	Leu	Ile
									35		40		45		
Pro	Ala	Pro	Gly	Asp	Tyr	Val	Thr	Ala	Lys	Met	Gly	Ile	Asp	Glu	Val
									50		55		60		
Ile	Val	Ser	Arg	Gln	Asn	Asp	Gly	Ser	Ile	Arg	Ala	Phe	Leu	Asn	Val
									65		70		75		80
Cys	Arg	His	Arg	Gly	Lys	Thr	Leu	Val	Ser	Val	Glu	Ala	Gly	Asn	Ala
									85		90		95		
Lys	Gly	Phe	Val	Cys	Ser	Tyr	His	Gly	Trp	Gly	Phe	Gly	Ser	Asn	Gly
									100		105		110		
Glu	Leu	Gln	Ser	Val	Pro	Phe	Glu	Lys	Asp	Leu	Tyr	Gly	Glu	Ser	Leu
									115		120		125		
Asn	Lys	Lys	Cys	Leu	Gly	Leu	Lys	Glu	Val	Ala	Arg	Val	Glu	Ser	Phe
									130		135		140		
His	Gly	Phe	Ile	Tyr	Gly	Cys	Phe	Asp	Gln	Glu	Ala	Pro	Pro	Leu	Met
									145		150		155		160
Asp	Tyr	Leu	Gly	Asp	Ala	Ala	Trp	Tyr	Leu	Glu	Pro	Met	Phe	Lys	His
									165		170		175		
Ser	Gly	Gly	Leu	Glu	Leu	Val	Gly	Pro	Pro	Gly	Lys	Val	Val	Ile	Lys
									180		185		190		
Ala	Asn	Trp	Lys	Ala	Pro	Ala	Glu	Asn	Phe	Val	Gly	Asp	Ala	Tyr	His
									195		200		205		
Val	Gly	Trp	Thr	His	Ala	Ser	Ser	Leu	Arg	Ser	Gly	Glu	Ser	Ile	Phe
									210		215		220		
Ser	Ser	Leu	Ala	Gly	Asn	Ala	Ala	Leu	Pro	Pro	Glu	Gly	Ala	Gly	Leu
									225		230		235		240
Gln	Met	Thr	Ser	Lys	Tyr	Gly	Ser	Gly	Met	Gly	Val	Leu	Trp	Asp	Gly
									245		250		255		
Tyr	Ser	Gly	Val	His	Ser	Ala	Asp	Leu	Val	Pro	Glu	Leu	Met	Ala	Phe
									260		265		270		
Gly	Gly	Ala	Lys	Gln	Glu	Arg	Leu	Asn	Lys	Glu	Ile	Gly	Asp	Val	Arg
									275		280		285		

4119

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<210> 27
<211> 2265
<212> DNA
<213> Artificial Sequence
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<220>
<223> A sequence encoding an NDO mutant.

tcagagcgtc	gttataagct	caatgaagcc	atgaacgaaa	acaacgaaaa	ttttcagcaa	1860
ctgaaagtto	gagttgagca	tcaactggat	ccgcaaaaact	ggggcaacag	cccgaaagctg	1920
cgctttactc	gctttatcac	caacgtccag	gccgcaatgg	acgtaaaatga	caaagagcta	1980
cttcacatcc	gctccaaacgt	cattctgcac	cgggcacgac	gtggcaatca	ggtcgatgtc	2040
tttacgccc	cccggaaaga	taaatggaaa	cgtggcgaag	gtggagtacg	aaaattggtc	2100
cagcgattcg	tcgattaccc	agagcgcata	cttcagacgc	acaatctgtat	ggtctttctg	2160
tgattcagtg	accattttta	caaatggtc	ctgcaaccgc	ggtcaccatt	aatcaaaggg	2220
aatgtacgtg	tatggcaat	caacaagtgc	tttcgataac	cggtg		2265

<210> 28

<211> 2265

<212> DNA

<213> Artificial Sequence

<220>

<223> A sequence encoding an NDO mutant.

<400> 28

gagggtagag	aaatcgaaatg	ccccttgcat	caaggctcggt	ttgacgtttgc	cacaggcaaa	60
gcctgtcg	cacccgtgac	acagaacatc	aaaacatatc	cagtcaagat	tgagaacctg	120
cgcgtatgc	ttgatttgc	ctaagaattt	taacaggagg	cacccgggc	cctagagcgt	180
aatcaccatcc	attccatctt	ttttaggtga	aaacatgaat	tacaataata	aaatcttggt	240
aagtgaatct	ggtctgagcc	aaaagcacct	gattcatggc	gttgaagaac	ttttccaaca	300
tgaactgaaa	accatttttgc	cgcggactgt	gtttttctc	actcatgata	gcctgattcc	360
tgccccccggc	gactatgttgc	ccgcaaaaat	ggggatttgc	gaggtcateg	tctccggca	420
gaacgcacgg	tcgattctgt	ctttctgaa	cgtttgcgg	catcggtggca	agacgctgg	480
gagcgtggaa	gccggcaatg	ccaaagggtt	tgtttgcgc	tatcacggct	ggggcttcgg	540
ctccaacgg	gaactgcaga	ggttccat	tgaaaaaagat	ctgtacggcg	agtcgctcaa	600
taaaaaatgt	ctgggggttgc	agaagtcgc	tcgcgtggag	agttccatg	gttcatcta	660
cgggtgc	gaccaggagg	cccttccttgc	tatggactat	ctgggtgc	ctgttggta	720
cctggaaac	atgttcaagg	atccggcg	tttagaactgc	gtcggtctc	caggcaaggt	780
tgtatcaag	gccaactgga	aggcaccggc	ggaaaaacttt	gtgggagatg	cataaccacgt	840
gggttggacg	cacgcgttgc	cggttcgtc	ggggggagtct	atcttcgt	cgctcgctgg	900
caatgcggcg	ctaccacatgc	aggcgcagg	tttgcataatg	acctccaaat	acggcagcgg	960
catgggtgt	tttgtggacg	gatattcagg	tgtgcata	cgagacttgg	ttccggaaatt	1020
gatggcattc	ggaggcgc	aaagcaggaa	gctgaacaaa	gaaatttggcg	atgttcgcgc	1080
tcggat	tcgcgcacc	tcaactgcac	cggttcccg	aacaacagca	tgctgacctg	1140
ctcggtgtt	ttcaaaatgt	ggaacccgat	cgacgcac	accacggagg	tctggaccta	1200
cgccattgtc	gaaaaagaca	tgcctgagg	tctcaagcgc	cggttggccg	actctgttca	1260
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cgggtggac	gtatacggcg	acgcggctca	tccaggcg	gtcggtcaat	cgccgatcg	1440
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ggttggat	gagcatgc	ctagacttg	gcataactgaa	tttacgaa	ctactgtatgc	1560
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tcagagcg	gttataagct	caatgaagcc	atgaacgaaa	acaacgaaaa	ttttcagcaa	1860
ctgaaagtgc	gagttgagca	tcaactggat	ccgcaaaaact	ggggcaacag	cccgaaagctg	1920
cgctttactc	gctttatcac	caacgtccag	gccgcaatgg	acgtaaaatga	caaagagcta	1980
cttcacatcc	gctccaaacgt	cattctgcac	cgggcacgac	gtggcaatca	ggtcgatgtc	2040
tttacgccc	cccggaaaga	taaatggaaa	cgtggcgaag	gtggagtacg	aaaattggtc	2100
cagcgattcg	tcgattaccc	agagcgcata	cttcagacgc	acaatctgtat	ggtctttctg	2160
tgattcagtg	accattttta	caaatggtc	ctgcaaccgc	ggtcaccatt	aatcaaaggg	2220
aatgtacgtg	tatggcaat	caacaagtgc	tttcgataac	cggtg		2265

<210> 29

<211> 2265

<212> DNA

<213> Artificial Sequence

<220>

<223> A sequence encoding an NDO mutant.

<400> 29		
gagggttagag aaatcgat ccccttgc cat caaggctgg ttgacgttt cacaggcaaa	60	
gccctgtgcg caccctgtac acagaacatc aaaacatc cagtcaagat tgagaacctg	120	
cgcgtaatga ttgatttgcg ctaagaattt taacaggagg caccctggc cctagagcgt	180	
aatcaccccc attccatctt ttttaggtga aaacatgaat tacaataata aaatcttgg	240	
aagtgaatct ggtctgagcc aaaagcacct gattcatggc gatgaagaac ttttccaaca	300	
tgaactgaaa accatttttgcg cgcggactg gcttttctc actcatgata gcctgattcc	360	
tgcccccggc gactatgtt cgcggaaaat ggggattgac gaggtcatcg tctccggca	420	
gaacgacggt tcgattcgtg ctttctgaa cgtttgcgg catcggtggca agacgctgg	480	
gagcgtggaa gccggcaatg coaaagggtt tgtttgcagc tattcacggct ggggcttcgg	540	
ctccaacggc gaactgcaga ggttccatt tgaaaaagat ctgtacggcg agtcgctcaa	600	
taaaaaatgt ctgggggtga aagaagtcgc tcgcgtggag agcttccatg gcttcatcta	660	
cgttgcctc gaccaggagg cccctccctc tatggactat ctgggtgacg ctgcttggta	720	
cctggAACCT atgttcaagc attccgggg ttttagaactg gtcggccctc caggcaaggt	780	
tgtgatcaag gccaactgga aggcacccggc ggaaaacttt gtgggagatg cataccacgt	840	
gggttggacg cacgcgtctt cgcttcgctc gggggagtc atcttctcg cgctcgctgg	900	
caatgcggcg ctaccacccgt aaggcgcagg cttgcaaaatg acctccaaat acggcagcgg	960	
catgggtgtg ttgtggacg gatattcagg tgcatacg gcagacttgg ttccggaaatt	1020	
gatggcattc ggaggcccaa agcaggaaag gctgaacaaa gaaattggcg atgttcgcgc	1080	
tcgatttat cgcagccacc tcaactgcac cgtttcccg aacaacagca tgctgacctg	1140	
ctcggtgtt ttcaagatg ggaacccgat cgacgcaaaac accaccggg tctggaccta	1200	
cgccattgtc gaaaaagaca tgccctgagga tctcaagcgc cgcttggccg actctgttca	1260	
gcaacgacc gggcctgtcg gcttctggga aagcgcacgac aatgacaata tggaaacagc	1320	
ttcgaaaaac ggcaagaataat atcaatcaag agatagtgtat ctgtttcaaa accttggttt	1380	
cggtagggac gtatacggcg aegcggctca tccaggcgtc gtggcaaat cggcgatcgg	1440	
cgagaccagt tatacggtt ttaccgggg ttaccaggca cacgtcagca gcttcaactg	1500	
ggctgagttc gagcatgcct cttagtacttg gcatactgaa cttacgagaactactgatcg	1560	
ctaacagacg agtcgaccat gatgatcaat attcaagaag acaagctgtt ttcccccac	1620	
gacgcccgaag agattttcg tttttcaat tgccacgact ctgcttgc aacaagaagcc	1680	
actacgctgc tgaccaggaa agcgcatttgg tggacatttggcttacccg tgcttggta	1740	
gagcaactgca gggggcaga ggtcaatattt caggtcattt cacgcgaact ggcgcagct	1800	
tcaagcggtc gttataagct caatgaagcc atgaacgttt acaacgaaaaa ttttcagcaa	1860	
ctgaaagttc gagttgagca tcaactggat ccgcggaaaact gggcaacag cccgaagctg	1920	
cgttttactc gctttatcac caacgtccag gcccgaatgg acgttaatgaa caaagagcta	1980	
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cagcgattcg tcgatttaccc agagcgcata cttcagacgc acaatctgtat ggtcttctg	2160	
tgattcgtg accatttttcaaaatggca ctgcaaccgc ggtcaccatt aatcaaaggaa	2220	
aatgtacgtg tatggcaat caacaagtgc ttgcataac cggtg	2265	

<210> 30

<211> 2265

<212> DNA

<213> Artificial Sequence

<220>

<223> A sequence encoding an NDO mutant.

<400> 30		
gagggttagag aaatcgat ccccttgc cat caaggctgg ttgacgttt cacaggcaaa	60	
gccctgtgcg caccctgtac acagaacatc aaaacatc cagtcaagat tgagaacctg	120	
cgcgtaatga ttgatttgcg ctaagaattt taacaggagg caccctggc cctagagcgt	180	
aatcaccccc attccatctt ttttaggtga aaacatgaat tacaataata aaatcttgg	240	
aagtgaatct ggtctgagcc aaaagcacct gattcatggc gatgaagaac ttttccaaca	300	
tgaactgaaa accatttttgcg cgcggactg gcttttctc actcatgata gcctgattcc	360	
tgcccccggc gactatgtt cgcggaaaat ggggattgac gaggtcatcg tctccggca	420	
gaacgacggt tcgattcgtg ctttctgaa cgtttgcgg catcggtggca agacgctgg	480	
gagcgtggaa gccggcaatg ccaaaagggtt tgtttgcagc tattcacggct ggggcttcgg	540	
ctccaacggc gaactgcaga gcgttccatt tgaaaaagat ctgtacggcg agtcgctcaa	600	

taaaaaatgt	ctgggggttga	aagaagtgc	tcgcgtggag	agcttccatg	gcttcatcta	660
cgggtgc	gaccaggagg	cccctcc	tatggactat	ctgggtgacg	ctgcgtggta	720
cctggAACCT	atgttcaagc	atccggcg	tttagaactg	gtcggtcc	caggcaaggt	780
tgtgatcaag	gccaactgga	aggcacccgc	ggaaaactt	gtgggagatg	cataaccacgt	840
gggttggacg	cacgcgtctt	cgttcgctc	gggggagtct	atcttctcg	cgctcgctgg	900
caatgcggcg	ctaccacctg	aaggcgcagg	cttgc当地atg	acctccaaat	acggcagcgg	960
catgggtgt	ttgtggacg	gatattcagg	tgtgc当地atg	gcagacttgg	ttccggaaatt	1020
gatggcattc	ggaggcgcaa	agcaggaaag	gtgaacaaa	gaaattggcg	atgttcgcgc	1080
tcgatttat	cgcagccacc	tcaactgcac	cgtttcc	acaacagca	tgctgacctg	1140
ctcgggtgtt	ttcaagat	ggaacccgat	cgacgcaa	accaccgagg	tctggaccta	1200
cgcattgtc	gaaaaagaca	tgcctgagga	tctcaagcgc	cgcttggcc	actctgttca	1260
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ttcgaaaaac	ggcaagaaat	atcaatcaag	agatagtat	ctgcttcaa	accttgg	1380
cggtagggac	gtatacggcg	acgcggtcta	tccaggcgtc	gtcggcaa	cggcgcgt	1440
cgagaccagt	tatcggtt	tctaccgggc	ttaccaggc	cacgtcagca	gtccaaactg	1500
ggctgagttc	gagcatgcct	ctagtacttg	gcatactgaa	cttacgaa	ctactgtatcg	1560
ctaacagacg	agtcgaccat	gtgtatcaat	attcaagaag	acaagctgt	ttccggccac	1620
gacgcccgaag	agattctcg	tttcttcaat	tgccacgact	ctgcttgc	acaagaagcc	1680
actacgctgc	tgaccaggaa	agcgcattt	ttggacattc	aggcttacc	tgcttgg	1740
gagcaactgc	ttgggtcaga	gttgcataat	caggctatt	cacgcgaact	gcgcgcagct	1800
tcagagcgtc	gttataagct	caatgaagcc	atgaacgtt	acaacgaaa	tttcagcaa	1860
ctgaaagttc	gagttgagca	tcaactggat	ccgc当地aaact	ggggcaacag	ccgc当地gt	1920
cgttttactc	gttttatc	caacgtccag	gccgcaatgg	acgttaatga	caaagagcta	1980
cttcacatcc	gttccaaacgt	cattctgcac	cgggcac	gtggcaatca	gttgc当地tgc	2040
tttacgccc	cccggaaaga	taaatggaa	cgtggcag	gtggagta	aaaattgg	2100
cagcgattcg	tcgattaccc	agagcgcata	ttcagacgc	acaatctgt	gttcttctg	2160
tgattcagt	accatttt	caaatgg	ctgcaaccgc	ggtcaccatt	aatcaaagg	2220
aatgtacgt	tatggcaat	caacaagtgc	ttcgataac	cggtg		2265

<210> 31

<211> 2265

<212> DNA

<213> Artificial Sequence

<220>

<223> A sequence encoding an NDO mutant.

<400> 31

gagggttag	aaatcgaaatg	ccccttgc	caaggcgg	ttgacgttt	cacaggcaaa	60
gcctgtcg	cacccgtgac	acagaacatc	aaaacatatc	cagtcaagat	tgagaac	120
cgcgtat	ttgatttgc	ctaagaattt	taacaggagg	cacccgggc	cctagagcgt	180
aatcacc	attccatctt	ttttaggt	aaacatgaat	tacaataata	aaatcttgg	240
aagtgaat	gttctgagcc	aaaagcacct	gattcatgc	gatgaagaac	ttttccaaca	300
tgaactgaa	accatttt	cgc当地actg	gcttttctc	actcatgata	gcctgattc	360
tgccccggc	gactatgtt	ccgc当地aaat	ggggattgac	gaggtcata	tctccggca	420
gaacgcgg	tcgattcgt	ctttctgaa	cg	catcg	ggc	480
gagcgtgg	gcccgc当地at	ccaaagg	tttgc	tatc	acgg	540
ctccaacgg	gaactgc	ggttccatt	tgaaaagat	ctgtacggc	agtcgctaa	600
taaaaaatgt	ctgggggtt	aaagaaagtgc	tcgc当地gg	agttccat	gttcatcta	660
cgggtgc	gaccaggagg	cccctcc	tatggactat	ctgggtgac	ctgc当地gg	720
cctggAACCT	atgttcaagc	atccggcg	tttagaactg	gtcggtcc	caggcaaggt	780
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gggttggacg	cacgcgtctt	cgttcgctc	gggggagtct	atcttctcg	cgctcgctgg	900
caatgcggcg	ctaccacctg	aaggcgcagg	cttgc当地atg	acctccaaat	acggcagcgg	960
catgggtgt	ttgtggacg	gatattcagg	tgtgc当地atg	gcagacttgg	ttccggaaatt	1020
gatggcattc	ggaggcgcaa	agcaggaaag	gtgaacaaa	gaaattggcg	atgttcgcgc	1080
tcggatttat	cgcagccacc	tcaactgcac	cgtttcc	acaacagca	tgctgacctg	1140
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cgcattgtc	gaaaaagaca	tgcctgagga	tctcaagcgc	cgcttggcc	actctgttca	1260
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ttcgaaaaac	ggcaagaaat	atcaatcaag	agatagtat	ctgcttcaa	accttgg	1380
cggtagggac	gtatacggcg	acgc当地tgc	tccaggcgtc	gtcggcaa	cggcgc当地gg	1440

cgagaccagt	tatcgagggtt	tctaccgggc	ttaccaggca	cacgtcagca	gctccaactg	1500
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ttctacgccc	cccgaaaaga	taaatggaaa	cgtggcgaag	gtggagtacg	aaaattggtc	2100
cagcgattcg	tcgattaccc	agagcgcata	cttcagacgc	acaatctgtat	ggtcttctg	2160
tgattcagtg	accatttt	caaataggta	ctgcaaccgc	ggtcaccatt	aatcaaagg	2220
aatgtacgtg	tatggcaat	caacaagtgc	tttcgataac	cggtg		2265

<210> 32

<211> 449

<212> PRT

<213> Artificial Sequence

<220>

<223> A polypeptide encoded by SEQ ID NO:27.

<400> 32

Met	Asn	Tyr	Asn	Asn	Lys	Ile	Leu	Val	Ser	Glu	Ser	Gly	Leu	Ser	Gln
1						5			10				15		
Lys	His	Leu	Ile	His	Gly	Asp	Glu	Glu	Leu	Phe	Gln	His	Glu	Leu	Lys
									20			25			30
Thr	Ile	Phe	Ala	Arg	Asn	Trp	Leu	Phe	Leu	Thr	His	Asp	Ser	Leu	Ile
									35			40			45
Pro	Ala	Pro	Gly	Asp	Tyr	Val	Thr	Ala	Lys	Met	Gly	Ile	Asp	Glu	Val
									50			55			60
Ile	Val	Ser	Arg	Gln	Asn	Asp	Gly	Ser	Ile	Arg	Ala	Phe	Leu	Asn	Val
									65			70			75
Cys	Arg	His	Arg	Gly	Lys	Thr	Leu	Val	Ser	Val	Glu	Ala	Gly	Asn	Ala
									85			90			95
Lys	Gly	Phe	Val	Cys	Ser	Tyr	His	Gly	Trp	Gly	Phe	Gly	Ser	Asn	Gly
									100			105			110
Glu	Leu	Gln	Ser	Val	Pro	Phe	Glu	Lys	Asp	Leu	Tyr	Gly	Glu	Ser	Leu
									115			120			125
Asn	Lys	Lys	Cys	Leu	Gly	Leu	Lys	Glu	Val	Ala	Arg	Val	Glu	Ser	Phe
									130			135			140
His	Gly	Phe	Ile	Tyr	Gly	Cys	Phe	Asp	Gln	Glu	Ala	Pro	Pro	Leu	Met
									145			150			155
Asp	Tyr	Leu	Gly	Asp	Ala	Ala	Trp	Tyr	Leu	Glu	Pro	Met	Phe	Lys	His
									165			170			175
Ser	Gly	Gly	Leu	Glu	Leu	Val	Gly	Pro	Pro	Gly	Lys	Val	Val	Ile	Lys
									180			185			190
Ala	Asn	Trp	Lys	Ala	Pro	Ala	Glu	Asn	Phe	Val	Gly	Asp	Ala	Tyr	His
									195			200			205
Val	Gly	Trp	Trp	Thr	His	Ala	Ser	Ser	Leu	Arg	Ser	Gly	Glu	Ser	Ile
									210			215			220
Ser	Ser	Leu	Ala	Gly	Asn	Ala	Ala	Leu	Pro	Pro	Glu	Gly	Ala	Gly	Leu
									225			230			240
Gln	Met	Thr	Ser	Lys	Tyr	Gly	Ser	Gly	Met	Gly	Val	Leu	Trp	Asp	Gly
									245			250			255
Tyr	Ser	Gly	Val	His	Ser	Ala	Asp	Leu	Val	Pro	Glu	Leu	Met	Ala	Phe
									260			265			270
Gly	Gly	Ala	Lys	Gln	Glu	Arg	Leu	Asn	Lys	Glu	Ile	Gly	Asp	Val	Arg
									275			280			285
Ala	Arg	Ile	Tyr	Arg	Ser	His	Leu	Asn	Cys	Thr	Val	Phe	Pro	Asn	Asn
									290			295			300

Ser Met Leu Thr Cys Ser Gly Val Phe Lys Val Trp Asn Pro Ile Asp
 305 310 315 320
 Ala Asn Thr Thr Glu Val Trp Thr Tyr Ala Ile Val Glu Lys Asp Met
 325 330 335
 Pro Glu Asp Leu Lys Arg Arg Leu Ala Asp Ser Val Gln Arg Thr Gly
 340 345 350
 Gly Pro Ala Gly Phe Trp Glu Ser Asp Asp Asn Asp Asn Met Glu Thr
 355 360 365
 Ala Ser Gln Asn Gly Lys Lys Tyr Gln Ser Arg Asp Ser Asp Leu Leu
 370 375 380
 Ser Asn Leu Gly Phe Gly Glu Asp Val Tyr Gly Asp Ala Val Tyr Pro
 385 390 395 400
 Gly Val Val Gly Lys Ser Ala Ile Gly Glu Thr Ser Tyr Arg Gly Phe
 405 410 415
 Tyr Arg Ala Tyr Gln Ala His Val Ser Ser Ser Asn Trp Ala Glu Phe
 420 425 430
 Glu His Ala Ser Ser Thr Trp His Thr Glu Leu Thr Lys Thr Thr Asp
 435 440 445
 Arg

<210> 33
 <211> 449
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> A polypeptide encoded by SEQ ID NO:28.

<400> 33
 Met Asn Tyr Asn Asn Lys Ile Leu Val Ser Glu Ser Gly Leu Ser Gln
 1 5 10 15
 Lys His Leu Ile His Gly Asp Glu Glu Leu Phe Gln His Glu Leu Lys
 20 25 30
 Thr Ile Phe Ala Arg Asn Trp Leu Phe Leu Thr His Asp Ser Leu Ile
 35 40 45
 Pro Ala Pro Gly Asp Tyr Val Thr Ala Lys Met Gly Ile Asp Glu Val
 50 55 60
 Ile Val Ser Arg Gln Asn Asp Gly Ser Ile Arg Ala Phe Leu Asn Val
 65 70 75 80
 Cys Arg His Arg Gly Lys Thr Leu Val Ser Val Glu Ala Gly Asn Ala
 85 90 95
 Lys Gly Phe Val Cys Ser Tyr His Gly Trp Gly Phe Gly Ser Asn Gly
 100 105 110
 Glu Leu Gln Ser Val Pro Phe Glu Lys Asp Leu Tyr Gly Glu Ser Leu
 115 120 125
 Asn Lys Lys Cys Leu Gly Leu Lys Glu Val Ala Arg Val Glu Ser Phe
 130 135 140
 His Gly Phe Ile Tyr Gly Cys Phe Asp Gln Glu Ala Pro Pro Leu Met
 145 150 155 160
 Asp Tyr Leu Gly Asp Ala Ala Trp Tyr Leu Glu Pro Met Phe Lys His
 165 170 175
 Ser Gly Gly Leu Glu Leu Val Gly Pro Pro Gly Lys Val Val Ile Lys
 180 185 190
 Ala Asn Trp Lys Ala Pro Ala Glu Asn Phe Val Gly Asp Ala Tyr His
 195 200 205
 Val Gly Trp Thr His Ala Ser Ser Leu Arg Ser Gly Glu Ser Ile Phe
 210 215 220
 Ser Ser Leu Ala Gly Asn Ala Ala Leu Pro Pro Glu Gly Ala Gly Leu
 225 230 235 240
 Gln Met Thr Ser Lys Tyr Gly Ser Gly Met Gly Val Leu Trp Asp Gly
 245 250 255

Tyr Ser Gly Val His Ser Ala Asp Leu Val Pro Glu Leu Met Ala Phe
 260 265 270
 Gly Gly Ala Lys Gln Glu Arg Leu Asn Lys Glu Ile Gly Asp Val Arg
 275 280 285
 Ala Arg Ile Tyr Arg Ser His Leu Asn Cys Thr Val Phe Pro Asn Asn
 290 295 300
 Ser Met Leu Thr Cys Ser Gly Val Phe Lys Val Trp Asn Pro Ile Asp
 305 310 315 320
 Ala Asn Thr Thr Glu Val Trp Thr Tyr Ala Ile Val Glu Lys Asp Met
 325 330 335
 Pro Glu Asp Leu Lys Arg Arg Leu Ala Asp Ser Val Gln Arg Thr Ala
 340 345 350
 Gly Pro Ala Gly Phe Trp Glu Ser Asp Asp Asn Asn Met Glu Thr
 355 360 365
 Ala Ser Gln Asn Gly Lys Lys Tyr Gln Ser Arg Asp Ser Asp Leu Leu
 370 375 380
 Ser Asn Leu Gly Phe Gly Glu Asp Val Tyr Gly Asp Ala Val Tyr Pro
 385 390 395 400
 Gly Val Val Gly Lys Ser Ala Ile Gly Glu Thr Ser Tyr Arg Gly Phe
 405 410 415
 Tyr Arg Ala Tyr Gln Ala His Val Ser Ser Ser Asn Trp Ala Glu Phe
 420 425 430
 Glu His Ala Ser Ser Thr Trp His Thr Glu Leu Thr Lys Thr Thr Asp
 435 440 445
 Arg

<210> 34
 <211> 449
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> A polypeptide encoded by SEQ ID NO:29.

<400> 34
 Met Asn Tyr Asn Asn Lys Ile Leu Val Ser Glu Ser Gly Leu Ser Gln
 1 5 10 15
 Lys His Leu Ile His Gly Asp Glu Glu Leu Phe Gln His Glu Leu Lys
 20 25 30
 Thr Ile Phe Ala Arg Asn Trp Leu Phe Leu Thr His Asp Ser Leu Ile
 35 40 45
 Pro Ala Pro Gly Asp Tyr Val Thr Ala Lys Met Gly Ile Asp Glu Val
 50 55 60
 Ile Val Ser Arg Gln Asn Asp Gly Ser Ile Arg Ala Phe Leu Asn Val
 65 70 75 80
 Cys Arg His Arg Gly Lys Thr Leu Val Ser Val Glu Ala Gly Asn Ala
 85 90 95
 Lys Gly Phe Val Cys Ser Tyr His Gly Trp Gly Phe Gly Ser Asn Gly
 100 105 110
 Glu Leu Gln Ser Val Pro Phe Glu Lys Asp Leu Tyr Gly Glu Ser Leu
 115 120 125
 Asn Lys Lys Cys Leu Gly Leu Lys Glu Val Ala Arg Val Glu Ser Phe
 130 135 140
 His Gly Phe Ile Tyr Gly Cys Phe Asp Gln Glu Ala Pro Pro Leu Met
 145 150 155 160
 Asp Tyr Leu Gly Asp Ala Ala Trp Tyr Leu Glu Pro Met Phe Lys His
 165 170 175
 Ser Gly Gly Leu Glu Leu Val Gly Pro Pro Gly Lys Val Val Ile Lys
 180 185 190
 Ala Asn Trp Lys Ala Pro Ala Glu Asn Phe Val Gly Asp Ala Tyr His
 195 200 205

Val Gly Trp Thr His Ala Ser Ser Leu Arg Ser Gly Glu Ser Ile Phe
 210 215 220
 Ser Ser Leu Ala Gly Asn Ala Ala Leu Pro Pro Glu Gly Ala Gly Leu
 225 230 235 240
 Gln Met Thr Ser Lys Tyr Gly Ser Gly Met Gly Val Leu Trp Asp Gly
 245 250 255
 Tyr Ser Gly Val His Ser Ala Asp Leu Val Pro Glu Leu Met Ala Phe
 260 265 270
 Gly Gly Ala Lys Gln Glu Arg Leu Asn Lys Glu Ile Gly Asp Val Arg
 275 280 285
 Ala Arg Ile Tyr Arg Ser His Leu Asn Cys Thr Val Phe Pro Asn Asn
 290 295 300
 Ser Met Leu Thr Cys Ser Gly Val Phe Lys Val Trp Asn Pro Ile Asp
 305 310 315 320
 Ala Asn Thr Thr Glu Val Trp Thr Tyr Ala Ile Val Glu Lys Asp Met
 325 330 335
 Pro Glu Asp Leu Lys Arg Arg Leu Ala Asp Ser Val Gln Arg Thr Thr
 340 345 350
 Gly Pro Ala Gly Phe Trp Glu Ser Asp Asp Asn Asn Met Glu Thr
 355 360 365
 Ala Ser Gln Asn Gly Lys Lys Tyr Gln Ser Arg Asp Ser Asp Leu Leu
 370 375 380
 Ser Asn Leu Gly Phe Gly Glu Asp Val Tyr Gly Asp Ala Val Tyr Pro
 385 390 395 400
 Gly Val Val Gly Lys Ser Ala Ile Gly Glu Thr Ser Tyr Arg Gly Phe
 405 410 415
 Tyr Arg Ala Tyr Gln Ala His Val Ser Ser Ser Asn Trp Ala Glu Phe
 420 425 430
 Glu His Ala Ser Ser Thr Trp His Thr Glu Leu Thr Lys Thr Thr Asp
 435 440 445
 Arg

<210> 35
 <211> 449
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> A polypeptide encoded by SEQ ID NO:30.

<400> 35
 Met Asn Tyr Asn Asn Lys Ile Leu Val Ser Glu Ser Gly Leu Ser Gln
 1 5 10 15
 Lys His Leu Ile His Gly Asp Glu Glu Leu Phe Gln His Glu Leu Lys
 20 25 30
 Thr Ile Phe Ala Arg Asn Trp Leu Phe Leu Thr His Asp Ser Leu Ile
 35 40 45
 Pro Ala Pro Gly Asp Tyr Val Thr Ala Lys Met Gly Ile Asp Glu Val
 50 55 60
 Ile Val Ser Arg Gln Asn Asp Gly Ser Ile Arg Ala Phe Leu Asn Val
 65 70 75 80
 Cys Arg His Arg Gly Lys Thr Leu Val Ser Val Glu Ala Gly Asn Ala
 85 90 95
 Lys Gly Phe Val Cys Ser Tyr His Gly Trp Gly Phe Gly Ser Asn Gly
 100 105 110
 Glu Leu Gln Ser Val Pro Phe Glu Lys Asp Leu Tyr Gly Glu Ser Leu
 115 120 125
 Asn Lys Lys Cys Leu Gly Leu Lys Glu Val Ala Arg Val Glu Ser Phe
 130 135 140
 His Gly Phe Ile Tyr Gly Cys Phe Asp Gln Glu Ala Pro Pro Leu Met
 145 150 155 160

Asp Tyr Leu Gly Asp Ala Ala Trp Tyr Leu Glu Pro Met Phe Lys His
 165 170 175
 Ser Gly Gly Leu Glu Leu Val Gly Pro Pro Gly Lys Val Val Ile Lys
 180 185 190
 Ala Asn Trp Lys Ala Pro Ala Glu Asn Phe Val Gly Asp Ala Tyr His
 195 200 205
 Val Gly Trp Thr His Ala Ser Ser Leu Arg Ser Gly Glu Ser Ile Phe
 210 215 220
 Ser Ser Leu Ala Gly Asn Ala Ala Leu Pro Pro Glu Gly Ala Gly Leu
 225 230 235 240
 Gln Met Thr Ser Lys Tyr Gly Ser Gly Met Gly Val Leu Trp Asp Gly
 245 250 255
 Tyr Ser Gly Val His Ser Ala Asp Leu Val Pro Glu Leu Met Ala Phe
 260 265 270
 Gly Gly Ala Lys Gln Glu Arg Leu Asn Lys Glu Ile Gly Asp Val Arg
 275 280 285
 Ala Arg Ile Tyr Arg Ser His Leu Asn Cys Thr Val Phe Pro Asn Asn
 290 295 300
 Ser Met Leu Thr Cys Ser Gly Val Phe Lys Val Trp Asn Pro Ile Asp
 305 310 315 320
 Ala Asn Thr Thr Glu Val Trp Thr Tyr Ala Ile Val Glu Lys Asp Met
 325 330 335
 Pro Glu Asp Leu Lys Arg Arg Leu Ala Asp Ser Val Gln Arg Thr Leu
 340 345 350
 Gly Pro Ala Gly Phe Trp Glu Ser Asp Asp Asn Asn Met Glu Thr
 355 360 365
 Ala Ser Gln Asn Gly Lys Tyr Gln Ser Arg Asp Ser Asp Leu Leu
 370 375 380
 Ser Asn Leu Gly Phe Gly Glu Asp Val Tyr Gly Asp Ala Val Tyr Pro
 385 390 395 400
 Gly Val Val Gly Lys Ser Ala Ile Gly Glu Thr Ser Tyr Arg Gly Phe
 405 410 415
 Tyr Arg Ala Tyr Gln Ala His Val Ser Ser Ser Asn Trp Ala Glu Phe
 420 425 430
 Glu His Ala Ser Ser Thr Trp His Thr Glu Leu Thr Lys Thr Thr Asp
 435 440 445
 Arg

<210> 36
 <211> 449
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> A polypeptide encoded by SEQ ID NO:31.

<400> 36
 Met Asn Tyr Asn Asn Lys Ile Leu Val Ser Glu Ser Gly Leu Ser Gln
 1 5 10 15
 Lys His Leu Ile His Gly Asp Glu Glu Leu Phe Gln His Glu Leu Lys
 20 25 30
 Thr Ile Phe Ala Arg Asn Trp Leu Phe Leu Thr His Asp Ser Leu Ile
 35 40 45
 Pro Ala Pro Gly Asp Tyr Val Thr Ala Lys Met Gly Ile Asp Glu Val
 50 55 60
 Ile Val Ser Arg Gln Asn Asp Gly Ser Ile Arg Ala Phe Leu Asn Val
 65 70 75 80
 Cys Arg His Arg Gly Lys Thr Leu Val Ser Val Glu Ala Gly Asn Ala
 85 90 95
 Lys Gly Phe Val Cys Ser Tyr His Gly Trp Gly Phe Gly Ser Asn Gly
 100 105 110

Glu Leu Gln Ser Val Pro Phe Glu Lys Asp Leu Tyr Gly Glu Ser Leu
 115 120 125
 Asn Lys Lys Cys Leu Gly Leu Lys Glu Val Ala Arg Val Glu Ser Phe
 130 135 140
 His Gly Phe Ile Tyr Gly Cys Phe Asp Gln Glu Ala Pro Pro Leu Met
 145 150 155 160
 Asp Tyr Leu Gly Asp Ala Ala Trp Tyr Leu Glu Pro Met Phe Lys His
 165 170 175
 Ser Gly Gly Leu Glu Leu Val Gly Pro Pro Gly Lys Val Val Ile Lys
 180 185 190
 Ala Asn Trp Lys Ala Pro Ala Glu Asn Phe Val Gly Asp Ala Tyr His
 195 200 205
 Val Gly Trp Thr His Ala Ser Ser Leu Arg Ser Gly Glu Ser Ile Phe
 210 215 220
 Ser Ser Leu Ala Gly Asn Ala Ala Leu Pro Pro Glu Gly Ala Gly Leu
 225 230 235 240
 Gln Met Thr Ser Lys Tyr Gly Ser Gly Met Gly Val Leu Trp Asp Gly
 245 250 255
 Tyr Ser Gly Val His Ser Ala Asp Leu Val Pro Glu Leu Met Ala Phe
 260 265 270
 Gly Gly Ala Lys Gln Glu Arg Leu Asn Lys Glu Ile Gly Asp Val Arg
 275 280 285
 Ala Arg Ile Tyr Arg Ser His Leu Asn Cys Thr Val Phe Pro Asn Asn
 290 295 300
 Ser Met Leu Thr Cys Ser Gly Val Phe Lys Val Trp Asn Pro Ile Asp
 305 310 315 320
 Ala Asn Thr Thr Glu Val Trp Thr Tyr Ala Ile Val Glu Lys Asp Met
 325 330 335
 Pro Glu Asp Leu Lys Arg Arg Leu Ala Asp Ser Val Gln Arg Thr Ile
 340 345 350
 Gly Pro Ala Gly Phe Trp Glu Ser Asp Asp Asn Asp Asn Met Glu Thr
 355 360 365
 Ala Ser Gln Asn Gly Lys Lys Tyr Gln Ser Arg Asp Ser Asp Leu Leu
 370 375 380
 Ser Asn Leu Gly Phe Gly Glu Asp Val Tyr Gly Asp Ala Val Tyr Pro
 385 390 395 400
 Gly Val Val Gly Lys Ser Ala Ile Gly Glu Thr Ser Tyr Arg Gly Phe
 405 410 415
 Tyr Arg Ala Tyr Gln Ala His Val Ser Ser Ser Asn Trp Ala Glu Phe
 420 425 430
 Glu His Ala Ser Ser Thr Trp His Thr Glu Leu Thr Lys Thr Thr Asp
 435 440 445
 Arg

<210> 37
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> A mutagenic oligonucleotide.

<400> 37
 ttcagcgaac ggtcgggcct gc

<210> 38
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>

<223> A tetracycline repair oligonucleotide.

<400> 38

gccggggcctc ttgcgggata tcgtcca

27

<210> 39

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> An ampicillin knockout oligonucleotide.

<400> 39

gttgccattg ctgcaggcat cgtggtg

27

<210> 40

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> A mutagenic oligonucleotide.

<400> 40

gaggcacccg cggaagcttt tgtgggagat gca

33

<210> 41

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> A mutagenic oligonucleotide.

<400> 41

gcaccccgccg aacaatttgt gggagatgca

30

<210> 42

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> A mutagenic oligonucleotide.

<400> 42

ccgcggaaag ctttgtggga g

21

<210> 43

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> A mutagenic oligonucleotide.

<400> 43

ccgcggaaaa gcttgtggga gatg

24

<210> 44

<211> 23

<212> DNA		
<213> Artificial Sequence		
<220>		
<223> A mutagenic oligonucleotide.		
<400> 44		
cgcgaaaaac gttgtgggag atg		23
<210> 45		
<211> 23		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> A mutagenic oligonucleotide.		
<400> 45		
atattcaggt gcgcatacg cag		23
<210> 46		
<211> 34		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> A mutagenic oligonucleotide.		
<400> 46		
ggacggatat tcagggctcc atagcgcaga cttg		34
<210> 47		
<211> 33		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> A mutagenic oligonucleotide.		
<400> 47		
gacggatatt caggtAACCA tagcgcagac ttg		33
<210> 48		
<211> 30		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> A mutagenic oligonucleotide.		
<400> 48		
ggtgtttca aagtgcgcAA cccgatcgac		30
<210> 49		
<211> 26		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> A mutagenic oligonucleotide.		
<400> 49		

ctgttcagcg aaacttcggg cctgct	26
<210> 50	
<211> 26	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> A mutagenic oligonucleotide.	
<400> 50	
ctgttcagcg aaggttcggg cctgct	26
<210> 51	
<211> 26	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> A mutagenic oligonucleotide.	
<400> 51	
ctgttcagcg aagcttcggg cctgct	26
<210> 52	
<211> 22	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> A mutagenic oligonucleotide.	
<400> 52	
ttcagcgaac gctcgggcct gc	22
<210> 53	
<211> 30	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> A mutagenic oligonucleotide.	
<400> 53	
ggcctgctgg cttcgccgaa agcgacgaca	30
<210> 54	
<211> 21	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> A mutagenic oligonucleotide.	
<400> 54	
gaaagcgacg ccaatgacaa t	21
<210> 55	
<211> 30	
<212> DNA	
<213> Artificial Sequence	

<220>

<223> A mutagenic oligonucleotide.

<400> 55

acgacaatga caattggaa acagcttcgc

30

<210> 56

<211> 2265

<212> DNA

<213> Artificial Sequence

<220>

<223> A sequence encoding an NDO mutant.

<400> 56

gagggttagag	aaatcgaatg	ccccttgc	cat	caaggtcgg	ttgacgtt	tg	cacaggcaaa	60
gccctgtgcg	cacccgtgac	acagaacatc	aaaacatatac	cagtcaagat	tgagaac	ctg		120
cgcgtaatga	ttgattttag	ctaagaattt	taacaggagg	caccccgggc	cctagagcgt			180
aatcacc	ccatctt	ttttaggtga	aaacatgaat	tacaataata	aaatcttgg			240
aagtgaatct	ggtctgagcc	aaaagcacct	gattcatggc	gatgaagaac	tttccaaca			300
tgaactgaaa	accatttttgc	cgcgaaactg	gtt	actcatgata	gcctgatt	cc		360
tgccccccggc	gactatgtt	ccgcaaaaat	ggggattgac	gaggtcatcg	tctccggca			420
gaacgacggt	tcgattcgt	cttttctgaa	cgtttgcgg	catcg	tggttgc	gca	agacgctgg	480
gagcgtggaa	gccggcaatg	ccaaagg	tttgc	tatcacgg	gggcttgc	gg		540
ctccaaacgg	gaa	cttgcaga	gctgttccatt	tgaaa	aaagat	ctgtacgg	gc	600
taaaaaatgt	ctgggg	ttgttgc	agaagtcgc	tcg	ctgg	tg	agtcgctaa	660
cgg	ttgttc	gaccaggagg	ccc	cttct	tat	ggactat	ctgggt	720
cctggaa	atgttca	atccgggg	ttt	gact	gtc	gg	tc	780
tgtgtatca	gcca	acttgg	aggc	cccc	gg	aaaactt	gtgg	840
gggttggacg	cac	gcgt	tct	cg	tttgc	gg	atgttgc	900
caat	atcc	cc	aggc	gc	tttgc	tttgc	tc	960
catgggtgt	ttt	gggg	ac	tttgc	tttgc	tttgc	tttgc	1020
gatgg	at	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	1080
tcgg	attt	tc	ggcc	ccacc	tttgc	tttgc	tttgc	1140
ctcgg	ttt	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	1200
cgccat	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	1260
gcca	ac	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	1320
gggc	cttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	1380
ttcg	caaa	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	1440
cgg	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	1500
cgag	acttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	1560
gg	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	1620
ctaa	ac	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	1680
gac	cc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	1740
acta	cgt	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	1800
gag	cact	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	1860
tc	at	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	1920
ctg	aa	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	1980
ctt	ttt	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	2040
ttt	ca	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	2100
cag	cgat	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	2160
tgat	tcg	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	2220
aat	ttt	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	2265

<210> 57

<211> 2265

<212> DNA

<213> Artificial Sequence

<220>

<223> A sequence encoding an NDO mutant.

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<210> 58
<211> 449
<212> PRT
<213> Artificial Sequence
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<220>
<223> A polypeptide encoded by SEQ ID NO:56.

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<400> 58
Met Asn Tyr Asn Asn Lys Ile Leu Val Ser Glu Ser Gly Leu Ser Gln
   1           5           10           15
Lys His Leu Ile His Gly Asp Glu Glu Leu Phe Gln His Glu Leu Lys
   20          25          30
Thr Ile Phe Ala Arg Asn Trp Leu Phe Leu Thr His Asp Ser Leu Ile
   35          40          45
Pro Ala Pro Gly Asp Tyr Val Thr Ala Lys Met Gly Ile Asp Glu Val
   50          55          60
Ile Val Ser Arg Gln Asn Asp Gly Ser Ile Arg Ala Phe Leu Asn Val
   65          70          75          80
Cys Arg His Arg Gly Lys Thr Leu Val Ser Val Glu Ala Gly Asn Ala
   85          90          95

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Lys Gly Phe Val Cys Ser Tyr His Gly Trp Gly Phe Gly Ser Asn Gly
 100 105 110
 Glu Leu Gln Ser Val Pro Phe Glu Lys Asp Leu Tyr Gly Glu Ser Leu
 115 120 125
 Asn Lys Lys Cys Leu Gly Leu Lys Glu Val Ala Arg Val Glu Ser Phe
 130 135 140
 His Gly Phe Ile Tyr Gly Cys Phe Asp Gln Glu Ala Pro Pro Leu Met
 145 150 155 160
 Asp Tyr Leu Gly Asp Ala Ala Trp Tyr Leu Glu Pro Met Phe Lys His
 165 170 175
 Ser Gly Gly Leu Glu Leu Val Gly Pro Pro Gly Lys Val Val Ile Lys
 180 185 190
 Ala Asn Trp Lys Ala Pro Ala Glu Asn Phe Val Gly Asp Ala Tyr His
 195 200 205
 Val Gly Trp Thr His Ala Ser Ser Leu Arg Ser Gly Glu Ser Ile Phe
 210 215 220
 Ser Ser Leu Ala Gly Asn Ala Ala Leu Pro Pro Glu Gly Ala Gly Leu
 225 230 235 240
 Gln Met Thr Ser Lys Tyr Gly Ser Gly Met Gly Val Leu Trp Asp Gly
 245 250 255
 Tyr Ser Gly Val His Ser Ala Asp Leu Val Pro Glu Leu Met Ala Phe
 260 265 270
 Gly Gly Ala Lys Gln Glu Arg Leu Asn Lys Glu Ile Gly Asp Val Arg
 275 280 285
 Ala Arg Ile Tyr Arg Ser His Leu Asn Cys Thr Val Phe Pro Asn Asn
 290 295 300
 Ser Met Leu Thr Cys Ser Gly Val Phe Lys Val Trp Asn Pro Ile Asp
 305 310 315 320
 Ala Asn Thr Thr Glu Val Trp Thr Tyr Ala Ile Val Glu Lys Asp Met
 325 330 335
 Pro Glu Asp Leu Lys Arg Arg Leu Ala Asp Ser Val Gln Arg Thr Trp
 340 345 350
 Gly Pro Ala Gly Phe Trp Glu Ser Asp Asp Asn Asn Met Glu Thr
 355 360 365
 Ala Ser Gln Asn Gly Lys Tyr Gln Ser Arg Asp Ser Asp Leu Leu
 370 375 380
 Ser Asn Leu Gly Phe Gly Glu Asp Val Tyr Gly Asp Ala Val Tyr Pro
 385 390 395 400
 Gly Val Val Gly Lys Ser Ala Ile Gly Glu Thr Ser Tyr Arg Gly Phe
 405 410 415
 Tyr Arg Ala Tyr Gln Ala His Val Ser Ser Ser Asn Trp Ala Glu Phe
 420 425 430
 Glu His Ala Ser Ser Thr Trp His Thr Glu Leu Thr Lys Thr Thr Asp
 435 440 445
 Arg

<210> 59
 <211> 449
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> A polypeptide encoded by SEQ ID NO:57.

<400> 59
 Met Asn Tyr Asn Asn Lys Ile Leu Val Ser Glu Ser Gly Leu Ser Gln
 1 5 10 15
 Lys His Leu Ile His Gly Asp Glu Glu Leu Phe Gln His Glu Leu Lys
 20 25 30
 Thr Ile Phe Ala Arg Asn Trp Leu Phe Leu Thr His Asp Ser Leu Ile
 35 40 45

Pro Ala Pro Gly Asp Tyr Val Thr Ala Lys Met Gly Ile Asp Glu Val
 50 55 60
 Ile Val Ser Arg Gln Asn Asp Gly Ser Ile Arg Ala Phe Leu Asn Val
 65 70 75 80
 Cys Arg His Arg Gly Lys Thr Leu Val Ser Val Glu Ala Gly Asn Ala
 85 90 95
 Lys Gly Phe Val Cys Ser Tyr His Gly Trp Gly Phe Gly Ser Asn Gly
 100 105 110
 Glu Leu Gln Ser Val Pro Phe Glu Lys Asp Leu Tyr Gly Glu Ser Leu
 115 120 125
 Asn Lys Lys Cys Leu Gly Leu Lys Glu Val Ala Arg Val Glu Ser Phe
 130 135 140
 His Gly Phe Ile Tyr Gly Cys Phe Asp Gln Glu Ala Pro Pro Leu Met
 145 150 155 160
 Asp Tyr Leu Gly Asp Ala Ala Trp Tyr Leu Glu Pro Met Phe Lys His
 165 170 175
 Ser Gly Gly Leu Glu Leu Val Gly Pro Pro Gly Lys Val Val Ile Lys
 180 185 190
 Ala Asn Trp Lys Ala Pro Ala Glu Asn Phe Val Gly Asp Ala Tyr His
 195 200 205
 Val Gly Trp Thr His Ala Ser Ser Leu Arg Ser Gly Glu Ser Ile Phe
 210 215 220
 Ser Ser Leu Ala Gly Asn Ala Ala Leu Pro Pro Glu Gly Ala Gly Leu
 225 230 235 240
 Gln Met Thr Ser Lys Tyr Gly Ser Gly Met Gly Val Leu Trp Asp Gly
 245 250 255
 Tyr Ser Gly Val His Ser Ala Asp Leu Val Pro Glu Leu Met Ala Phe
 260 265 270
 Gly Gly Ala Lys Gln Glu Arg Leu Asn Lys Glu Ile Gly Asp Val Arg
 275 280 285
 Ala Arg Ile Tyr Arg Ser His Leu Asn Cys Thr Val Phe Pro Asn Asn
 290 295 300
 Ser Met Leu Thr Cys Ser Gly Val Phe Lys Val Trp Asn Pro Ile Asp
 305 310 315 320
 Ala Asn Thr Thr Glu Val Trp Thr Tyr Ala Ile Val Glu Lys Asp Met
 325 330 335
 Pro Glu Asp Leu Lys Arg Arg Leu Ala Asp Ser Val Gln Arg Thr Tyr
 340 345 350
 Gly Pro Ala Gly Phe Trp Glu Ser Asp Asp Asn Asp Asn Met Glu Thr
 355 360 365
 Ala Ser Gln Asn Gly Lys Lys Tyr Gln Ser Arg Asp Ser Asp Leu Leu
 370 375 380
 Ser Asn Leu Gly Phe Gly Glu Asp Val Tyr Gly Asp Ala Val Tyr Pro
 385 390 395 400
 Gly Val Val Gly Lys Ser Ala Ile Gly Glu Thr Ser Tyr Arg Gly Phe
 405 410 415
 Tyr Arg Ala Tyr Gln Ala His Val Ser Ser Ser Asn Trp Ala Glu Phe
 420 425 430
 Glu His Ala Ser Ser Thr Trp His Thr Glu Leu Thr Lys Thr Thr Asp
 435 440 445
 Arg

<210> 60
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> A mutagenic oligonucleotide.

<400> 60

gttcagcgaa cgggcgggccc tgctgg 26
<210> 61
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> A mutagenic oligonucleotide.

<400> 61
gttcagcgaa cggccgggccc tgctgg 26
<210> 62
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> A mutagenic oligonucleotide.

<400> 62
gttcagcgaa cgaccgggccc tgctgg 26
<210> 63
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> A mutagenic oligonucleotide.

<400> 63
gttcagcgaa cgatcgggccc tgctgg 26
<210> 64
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> A mutagenic oligonucleotide.

<400> 64
gttcagcgaa cgtggggggccc tgctgg 26
<210> 65
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> A mutagenic oligonucleotide.

<400> 65
ttcagcgaaac gtacgggcct gctgg 25